

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 26, 2006, 23:22:24 ; Search time 302 Seconds
(without alignments)
1219.060 Million cell updates/sec

Title: US-10-501-930-1

Perfect score: 2102

Sequence: 1 MRSGGTFLALIGSLMLLLL.....MLQLHMRGILKLPFSKQETA 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2102	100.0	398	1	Q84t1 mus musculus
2	2102	100.0	405	2	Q3t9n4 mus musculus
3	1936	92.1	398	2	Q6zxc7 rattus norv
4	1922	91.4	362	2	Q8bi43 mus musculus
5	1772	84.3	398	1	P61647 homo sapien
6	1772	84.3	398	1	Q5vzh4 homo sapien
7	1763	83.9	398	1	P61648 pan troglod
8	1597	76.0	398	2	Q5ndg0 bos taurus
9	1183	56.3	398	2	Q6zxc6 gallus gall
10	728	34.6	343	2	Q6kco2 brachydanio
11	727.5	34.6	379	2	Q6kco0 tetraodon n
12	725.5	34.5	378	2	Q5k019 oryziat lat
13	719.5	34.2	372	2	Q50j40 fugu rubrip
14	719.5	34.2	379	2	Q6kco1 fugu rubrip
15	715.5	34.0	356	2	Q6kb27 brachydanio
16	710.5	33.8	342	2	P79783 gallus gall
17	703	33.4	356	1	P61642 pan troglod
18	702	33.4	342	2	Q78ei9 rattus sp.
19	701	33.3	356	2	P70554 rattus norv
20	700	33.3	356	1	Q92185 homo sapien
21	700	33.3	356	2	Q6zxc2 bos taurus
22	700	33.3	412	1	P70126 mus musculus
23	699.5	33.3	370	2	Q6kb28 fugu rubrip
24	697	33.2	355	2	Q8bl76 mus musculus
25	697	33.2	355	2	Q8klc1 mus musculus
26	692	32.9	376	2	Q3trw3 mus musculus
27	691	32.9	355	2	Q8bw10 mus musculus
28	689	32.8	341	2	Q64468 mus musculus
29	688	32.7	376	2	Q8jzq3 mus musculus
30	687.5	32.7	359	2	Q6zxa0 xenopus lae
31	686	32.6	374	2	Q5ndf9 bos taurus

32	686	32.6	376	1	SIABF_PANTR	P61646 pan troglod
33	686	32.6	376	2	Q6zxc7 RAT	Q6zxc7 rattus norv
34	686	32.6	376	2	Q6zxc8 RAT	Q6zxc8 rattus norv
35	685	32.5	419	2	Q4SU01_TETNG	Q4su01 tetraodon n
36	682.5	32.5	338	2	Q6WR01_XENLA	Q6wr01 xenopus lae
37	682	32.4	355	1	SIABF_MOUSE	Q64687 mus musculus
38	678	32.3	376	2	Q6zxc8_CHICK	Q6zxc8 gallus gall
39	677.5	32.2	345	2	Q6Dn96_XENTR	Q6dng6 xenopus tro
40	677	32.2	376	1	SIABF_HUMAN	O15466 homo sapien
41	674.5	32.1	275	2	Q3V301_MOUSE	Q3v3b1 mus musculus
42	670	31.9	369	2	Q6kb29_FUGRU	Q6kb29 fugu rubrip
43	665.5	31.7	288	2	Q50J35_BRARE	Q50j35 brachydanio
44	665.5	31.7	298	2	Q4T001_TETNG	Q4t001 tetraodon n
45	654.5	31.1	335	2	Q6Kc12_TETNG	Q6kc12 tetraodon n

ALIGNMENTS

RESULT 1

SIABF_MOUSE STANDARD; P61646; 398 AA.
AC Q84t1;
DT 01-JUN-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Alpha-2,8-sialyltransferase 8F (EC 2.4.99.-) (ST8Sia VI).
GN Name=St8sia6; Synonyms=St8f;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
RZ NUCLEOTIDE SEQUENCE [MRNA], AND CHARACTERIZATION.
RX MEDLINE=22086185; PubMed=1198089; DOI=10.1074/jbc.M112367200;
RA Takahima S., Ishida H.K., Inazu T., Ando T., Ishida H., Kiso M.,
Teuji S., Teujimoto M.;
RT "Molecular cloning and expression of a sixth type of alpha 2,8-sialyltransferase (ST8Sia VI) that sialylates O-glycans."
RL J. Biol. Chem. 277:24030-24038(2002).
CC -!- FUNCTION: Prefers O-glycans as N-glycans or glycolipids as acceptor substrates. The minimal acceptor substrate is the NeuAc-alpha-2,3(6)-Gal sequence at the nonreducing end of their carbohydrate groups.
CC -!- PATHWAY: Glycosylation.
CC -!- SUBCELLULAR LOCATION: Golgi apparatus; Golgi membrane; single-pass type II membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the glycosyltransferase 29 family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonCommercial License
CC ENBL; AB059554; BAC01265.1; -; mRNA.
CC Ensembl; ENSMUSG0000003418; Mus musculus.
CC MGI; MGI:2386797; st8sia6.
CC GO; GO:0008373; F:sialyltransferase activity; IDA.
CC GO; GO:0016051; P:carbohydrate biosynthesis; IDA.
CC GO; GO:0009247; P:glycolipid biosynthesis; IDA.
CC GO; GO:0006493; P:protein amino acid O-linked glycosylation; IDA.
CC InterPro; IPR001675; Glyco trans 29.
CC InterPro; IPR012163; Sialyl trans 1.
CC Pfam; PF00777; Glyco transf 29; .
CC PRSF; PRSF005557; Sialyl trans 1.
KW Glycoprotein; Glycosyltransferase; Golgi stack; Membrane; Signal-anchor; Transferase; Transmembrane.
CHAIN 1 398 Alpha-2,8-sialyltransferase 8F.
FTOPO_DOM 1 3 Cytoplasmic (Potential).
FTTRANSMEM 4 24 Signal-anchor for type II membrane protein (Potential).
FTOPO_DOM 25 398 Luminal (Potential).
FTCARBOHYD 65 66 N-linked (GlcNAc...) (Potential).

RN RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen; DOI=10.1038/35055500; MEDLINE=21085660; PubMed=11217851; Itoh M., Itoh M., Ishii Y.,
 RX Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Itoh M., Itoh M.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsumoto H., Aashburner M., Batalov S., Casavant T.,
 RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staebli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gutencich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [6]
 RN RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen; DOI=10.1101/gr.145100; MEDLINE=20499378; PubMed=11042159; Itoh M., Itoh M.,
 RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RN RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen; DOI=10.1101/gr.152600; MEDLINE=20530913; PubMed=11076861; Itoh M., Itoh M.,
 RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RN RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Activated spleen; DOI=10.1093/glycob/cw1063; PubMed=15843597; DOI=10.1093/glycob/cw1063; Delannoy P., Oriol R.,
 RX Harduin-Lepers A., Mollicone R., Delannoy P., Oriol R.;
 RA "The animal sialyltransferases and sialyltransferase-related genes: a
 phylogenetic approach.";
 RL Glycobiology 15:805-817(2005).
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 CC -----
 CC EMBL; AKJ72400; BAE42986.1; -; mRNA.
 DR MG1; MG12386797; st8sia6.
 DR GO; GO:0008373; F:sialyltransferase activity; IEA.
 DR GO; GO:0016051; P:carbohydrate biosynthesis; IEA.
 DR GO; GO:0009247; P:glycolipid biosynthesis; IEA.
 DR GO; GO:0006493; P:protein amino acid O-linked glycosylation; IEA.
 DR InterPro; IPR001675; Glyco trans_29.
 DR InterPro; IPR012163; Sialyl trans_1.
 DR Pfam; PF00777; Glyco trans_29; 1.
 DR PIRSF; PIRSF005557; Sialyl trans_1.
 KW Glycosyltransferase, Transferase.
 SQ SEQUENCE 405 AA; 46323 MW; 48B7A17BE3443487 CRC64;
 Query Match 92.1%; Score 1936; DB 2; Length 398;
 Query Match 100.0%; Score 2102; DB 2; Length 405;
 Best Local Similarity 100.0%; P-adj. No. 2.5e-156; Indels 0; Gaps 0;
 Matches 398; Conservative 0; Mismatches 0;
 QY 1 MRSGGTIFALIGSLMLLLLRMLPCPADAPARSRLMEGSRDTSGLTSAALKTLWSPPTP 60
 DB 1 MRSGGTIFALIGSLMLLLLRMLPCPADAPARSRLMEGSRDTSGLTSAALKTLWSPPTP 60
 QY 61 VPRTRNSTYDEKTTQTEKCKIYSLNSLNKTRYSDDYLTQITNIORCPWNRQAE 120
 DB 61 VPRTRNSTYDEKTTQTEKCKIYSLNSLNKTRYSDDYLTQITNIORCPWNRQAE 120
 QY 121 EYDNFRKLASCDAIODFVVSQNTVPVTGNTMSVEVSKKHIPRENIHFHFPVQPFVD 180
 DB 121 EYDNFRKLASCDAIODFVVSQNTVPVTGNTMSVEVSKKHIPRENIHFHFPVQPFVD 180
 QY 181 YPNQCAVGVNGGILNKLSCGAEKSDSFVRCNLPPITGSASKDVGSKTNLVTNPSII 240
 DB 181 YPNQCAVGVNGGILNKLSCGAEKSDSFVRCNLPPITGSASKDVGSKTNLVTNPSII 240
 QY 241 TLKYQNLKSKKAQFLEIDISTYGIIFLLPAPSVRANTGISPKYQTLKESKORQKVLFPFH 300
 DB 241 TLKYQNLKSKKAQFLEIDISTYGIIFLLPAPSVRANTGISPKYQTLKESKORQKVLFPFH 300
 QY 301 PLYRLHALFWRTKGVTAFLSLSLMTASVAVELCENVKLYGFWFPFSKTIETDPLSHHY 360
 DB 301 PLYRLHALFWRTKGVTAFLSLSLMTASVAVELCENVKLYGFWFPFSKTIETDPLSHHY 360
 QY 361 DNMLPKHGFHMQPKYSQMLQLFIRGILKLQFSKCEA 398
 DB 361 DNMLPKHGFHMQPKYSQMLQLFIRGILKLQFSKCEA 398
 RESULT 3
 Q6ZXC7 RAT PRELIMINARY; PF0; 398 AA.
 AC Q6ZXC7; 2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Alpha-2,8-sialyltransferase.
 GN Names:SIAT8F;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Mammalia; Rodentia; Sciurognathi;
 OC Mammalia; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague Dawley; DOI=10.1093/glycob/cw1063; PubMed=15843597; DOI=10.1093/glycob/cw1063; Delannoy P., Oriol R.,
 RX Harduin-Lepers A., Mollicone R., Delannoy P., Oriol R.;
 RA "The animal sialyltransferases and sialyltransferase-related genes: a
 phylogenetic approach.";
 RL Glycobiology 15:805-817(2005).
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 CC -----
 CC EMBL; AJ699423; CAG27885.1; -; mRNA.
 DR Ensembl; ENSRNOG00000018171; Rattus norvegicus.
 DR GO; GO:0008373; C:integral to Golgi membrane; IEA.
 DR GO; GO:0008373; F:sialyltransferase activity; IEA.
 DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
 DR InterPro; IPR001675; Glyco trans_29.
 DR InterPro; IPR012163; Sialyl trans_1.
 DR Pfam; PF00777; Glyco trans_29; 1.
 DR PIRSF; PIRSF005557; Sialyl trans_1.
 KW Glycosyltransferase, Transferase.
 SQ SEQUENCE 398 AA; 45271 MW; 8B06509DD781E06 CRC64;
 Query Match 92.1%; Score 1936; DB 2; Length 398;

Best Local Similarity 90.5%; Pred. No. 2.6e-143;
Matches 360; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

QY 1 MRSGGTFLALIGLMLLLMLLWCPADAPARSRLLMEGSRDTSATKLTWSPPTP 60
DB 1 MRPGGTLFALVGSIMLLLLLRWCPADAPARSRMLGEESREETGGTSAALKTLWSPPTP 60
QY 61 VPRTRNSTYLDKTTQTEKCKQLQVLSLSKTRRYSEDDYKLTQITNITQRCFWRQAE 120
DB 61 VPRTRNSTYLDKTPETAERCKGLKYSLSLANKTRRYSEDDYKLTQITNITQRCFWRQAE 120
QY 121 EYDNFRKALASCCDAQDFVVSQNTPVGTNMSVEVESKHIPIRENIHFMPVPSOPFVD 180
DB 121 EYDNFRKALASCCDAQDFVVSQNTPVGTNMSVEVESKHIPIRENIHFMPVPSOPFVD 180
QY 181 YPNQCAVGVNGGILNKSCLGAEIDKSDFFVRCNLPLPITGSASQDVGSKTNLTVNPSII 240
DB 181 YPNQCAVGVNGGILNKSCLGAEIDKSDFFVRCNLPLPITGSASQDVGSKTNLTVNPSII 240
QY 241 TLKYQNLKEKKAQFLIEDISTYGFDAFLPAPFSTRANTGIFSKYQTLTKESKQKVLFFH 300
DB 241 TLKYQNLKEKKAQFLIEDISAYGDAFLPAPFSTRANTGIFSKYQTLTKESKQKVLFFH 300
QY 301 PRYLRLHALFWRTKGYTAYELSTGLMTASVAVELCENVLYGFWPFSKTTLEDPLSHYY 360
DB 301 PRYLRLHALFWRTKGYTAYELSTGLMTASVAVELCENVLYGFWPFSKTTLEDPLSHYY 360
QY 361 DNMLPKHGFHOMPEKYSQMLQHLHMGILKLOFCKCETA 398
DB 361 DNMLPKHGFHOMPEKYSQMLQHLHMGILKLOFCKCETA 398

RESULT 4
Q8BI43 MOUSE
ID Q8BI43_MOUSE PRELIMINARY; PRT; 362 AA.
AC Q8BI43_MOUSE
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DE 07-FEB-2006, entry version 21.
DE 13 days embryo lung cDNA, RIKEN full-length enriched library,
DE clone:D430037E10 product:weakly similar to SIALYLTRANSFERASE 8.
GN Name:stebia6; Synonyms=Stat8f;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning."
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RC MEDLINE=16141072; DOI=10.1126/science.1112014;
RX Carninci P., Katayama T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Allen J.E.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailely T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli G., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,

RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishi G., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reid J., Reid J.P., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sander C., Sano S., Sessa L., Sheng Y.,
RA Schonbach C., Sekiguchi K., Sempel C., Silva D., Sinclair B.,
RA Shibata Y., Shimada H., Shimada S., Sultana R., Takenaka Y., Taki K.,
RA Sperling S., Stupka E., Sugura T., Tammela K., Tan S.L., Tang S., Tiedt R., Tiedt R., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Vesta S., Zimmer A., Hide W., Bult C.,
RA Yamanishi H., Zabarovsky E., Zhu S., E.T., Brusic V., Quackenbush J.,
RA Grimmond S.M., Tassadaq R.D., Li D.A., Kai C., Sasaki D., Tomaru Y.,
RA Wahlestedt C., Mattick J.S., Hum Suzuki M., Aoki J., Arakawa T.,
RA Fukuda S., Kanamori-Katayama M., Tida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawahina T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Hibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watanabe C., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RC PubMed=16141073; DOI=10.1126/science.1112009;
RX RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RC MEDLINE=22354683; PubMed=1246685;
RX Okazaki Y., Furuno M., Kasukawa N., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Mogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Shriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer J.S.,
RA Gaasterland T., Gariboldi M., Giesler T., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sander C., Schneider C., Sempel C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimin A., Carninci P., Hayatsu N.,
RA Hirokawa N., Katayama T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Kawasawa K., Arakawa T., Fukuda I.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Yang I., Zimin A., Carninci P., Hayatsu N.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RC MEDLINE=21085660; PubMed=1121785;
RX Kawai J., Shinagawa A., Shibata K., Kawai T., Hara A., Fukunishi Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wegner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RC MEDLINE=2050913; PubMed=11076861; DOI=10.1101/gr.152600;
RX Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitounai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hangaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kohji Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the ENBL/GenBank/DBJ databases.
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CC
CC -----
CC ENBL; AK085105; BAC39367.1; -, mRNA.
CC Ensembl; ENSMUSG0000003418; Mus musculus.
CC MGI; MGI:2386797; st8sia6.
CC MGI; MGI:2386797; st8sia6.
CC GO; GO:0008373; P:carbohydrate biosynthesis; IDA.
CC GO; GO:0016051; P:carbohydrate biosynthesis; IDA.
CC GO; GO:0009247; P:glycolipid biosynthesis; IDA.
CC GO; GO:0006493; P:protein amino acid O-linked glycosylation; IDA.
CC InterPro; IPR001675; Glyco trans. 29.
CC InterPro; IPR012163; Sialyl trans.
CC Pfam; PF00777; Glyco transf. 29; 1.
CC PIRSF; PIRSF005557; Sialyl trans; 1.
CC Glycosyltransferase; Transf. 1.
CC SQ SEQUENCE 362 AA; 41488 MW; 2C2530811ADB2788 CRC64;

Query Match 91.4%; Score 1922; DB 2; Length 362;
Best Local Similarity 100.0%; P.ead. No. 2.9e-142;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 37 MEGSREDTSGTSAALKTLWSPTVPVTRNSTRYLDEKTTQITEKCKDLOYSLSNLSNKTTR 96
Db 1 MEGSREDTSGTSAALKTLWSPTVPVTRNSTRYLDEKTTQITEKCKDLOYSLSNLSNKTTR 60
Qy 97 RYSEDDYLOITNIQRCFPMNRQSEYDNFRKAKSCCDAIODFVVSQNNTPVGTNMSYEV 156
Db 61 RYSEDDYLOITNIQRCFPMNRQSEYDNFRKAKSCCDAIODFVVSQNNTPVGTNMSYEV 120
Qy 157 ESKKHIPIRENIFMFPVSQPFQYPYNQCAVGVNGGILNKSLSGAEIDKSDFFRCNLP 216
Db 121 ESKKHIPIRENIFMFPVSQPFQYPYNQCAVGVNGGILNKSLSGAEIDKSDFFRCNLP 180
Qy 217 PITGSASKDVGSKTNLTVNPSLTLYQNLKKEKAQFLEDISTYGDALFLLLPAPSYRAN 276
Db 181 PITGSASKDVGSKTNLTVNPSLTLYQNLKKEKAQFLEDISTYGDALFLLLPAPSYRAN 240
Qy 277 TGISPKYQYQTLKSKMRQKVLFPYRLRHLLFWRTKGVTAIYLSLGLMTIASVAVELCE 336
Db 241 TGISPKYQYQTLKSKMRQKVLFPYRLRHLLFWRTKGVTAIYLSLGLMTIASVAVELCE 300
Qy 337 NVKLYGFWPFSKTIEDTPLSHHTDNMLPKHGHOMPKYSOMLQHLHMRGILKLOFSKCE 396
Db 301 NVKLYGFWPFSKTIEDTPLSHHTDNMLPKHGHOMPKYSOMLQHLHMRGILKLOFSKCE 360
Qy 397 TA 398
Db 361 TA 362
RESULT 5
SIA8F HUMAN
ID SIA8F HUMAN STANDARD; PIR; 398 AA.
AC P61647;
DT 07-JUN-2004, integrated into UniprotKB/Swiss-Prot.
DT 07-JUN-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Alpha-2, 8-sialyltransferase 8F
GN Name=ST8SIA6; Synonyms=SIAT8F;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RA Teinturier-Jelievre M., Delannoy P., Harduin-Lepers A.;
RT "Molecular cloning and expression of a sixth human alpha2,8-
RT sialyltransferase (hST8SIAVI)."
RL Submitted (JAN-2004) to the ENBL/GenBank/DBJ databases.
CC -I- FUNCTION: Prefers O-glycans O N-glycans or glycolipids as
CC acceptor substrates. The minimal acceptor substrate is the NeuAc-
CC alpha-2,3(6)-Gal sequence at the nonreducing end of their
CC carbohydrate groups (by similarity).
CC -I- PATHWAY: Glycosylation.
CC -I- SUBCELLULAR LOCATION: Golgi apparatus; Golgi membrane; single-pass
CC type II membrane protein (Probable).
CC -I- SIMILARITY: Belongs to the glycosyltransferase 29 family.
CC
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CC
CC -----
CC ENBL; AJ621583; CAP21722.1; -, mRNA.
CC Ensembl; ENSG00000148488; Homo sapiens.
CC HGNC; HGNC:23317; ST8SIA6.
CC InterPro; IPR001675; Glyco trans. 29.
CC InterPro; IPR012163; Sialyl trans.
CC Pfam; PF00777; Glyco transf. 29; 1.
CC PIRSF; PIRSF005557; Sialyl trans; 1.
CC Glycoprotein; Glycosyltransferase; Golgi stack; Membrane;
KW

KM Signal-anchor; Transferrase; Transmembrane.
 FT CHAIN 1 398 Alpha-2,8-sialyltransferase 8F.
 FT /Frida-PRO_0000149299.
 FT TOPO_DOM 1 3 Cytoplasmic (Potential).
 FT TRANSMEM 4 24 Signal-anchor for type II membrane
 FT protein (Potential).
 FT TOPO_DOM 25 398 Luminal (Potential).
 FT CARBOHYD 66 66 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 196 196 N-linked (GlcNAc...) (Potential).
 FT DISULFID 186 335 By similarity.
 FT SEQUENCE 398 AA; 44836 MW; 48F58B82E4B69A26 CRC64;
 SQ
 Query Match 84.3%; Score 1772; DB 1; Length 398;
 Best Local Similarity 82.7%; Pred. No. 2e-130;
 Matches 329; Conservative 30; Mismatches 39; Indels 0; Gaps 0;
 QY 1 MRSGGTLFALIGSLMLLLRLMPCADAPARSRLMEGSRDTSATKLTLMSPPTP 60
 DB 1 MRPGGALLALLALLLLLLRLMPCADAPGRARILVEESREATHGTPAALRTLRSPATA 60
 QY 61 VPRTRNSTYLDKTTQITEKCKDQYSLNSLNKTRRYSEDDYLOITITNIQRCPMNRQAE 120
 DB 61 VPRATNSTYLNKSLQITEKCKNQYIESFSNKTGYSNDYLOITIDQSCPWKQAE 120
 QY 121 EYDNFRKLASCDDAQDFVVSQNTPVGTNNMSYEVEKSHPIRENIHMFVPVSPFVD 180
 DB 121 EYANFRKLASCDDAQDFVVSQNTPVGTNNMSYEVEKSHPIRENIHMFVPVSPFVD 180
 QY 181 YPNQCAVVGNGGILNKSICGAEIDSDVFRCNLPPTTGSASKQVGSKTNLVTNPSII 240
 DB 181 YPNQCAVVGNGGILNKSICGTEIDSDVFRCNLPPTTGDVSKQVGSKTNLVTNPSII 240
 QY 241 TLKYONLKEKKAQFLEDISTYGDALFLLPAPSFYRANTGTSFKVYQTLKESKQKVLFFH 300
 DB 241 TLKYGNLKEKKAFLIEDIATYGDALFLLPAPSFYRANTGTSFKVYTLLESKARQKVLFFH 300
 QY 301 PRLRHALLFWRTKGTAVYRLSTGLMIASVAVELCNVLYGFWPFSKTIEDTFLSHHHY 360
 DB 301 PKYLDLALFWRTKGTAVYRLSTGLMITSVAVELCNVLYGFWPFSKTIEDTIPVSHHHY 360
 QY 361 DNKLPHGHQHPKQKYSQILQHLKMGKGLLKQFSKCEVA 398
 DB 361 DNKLPHGHQHPKQKYSQILQHLKMGKGLLKQFSKCEVA 398

RESULT 6
 QSVZH4 HUMAN PRELIMINARY; PR; 398 AA.
 ID QSVZH4; AC QSVZH4;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Likely ortholog of mouse sialyltransferase 8-VI (Alpha-2, 8-sialyltransferase) (ST8SIA-VI).
 GN Name=RP11-414K1.1; ORFNames=RP11-414K1.1-001;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP Heath P.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Pearce A.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AL158164; CAI40658.1; -; Genomic_DNA.
 DR EMBL; AL160289; CAI40658.1; JOINED; Genomic_DNA.
 DR EMBL; AL160289; CAH70722.1; -; Genomic_DNA.
 DR EMBL; AL158164; CAH70722.1; JOINED; Genomic_DNA.
 DR Ensembl; ENSG00000148488; Homo sapiens.
 DR HGNC; HGNC:23317; ST8SIA6.
 DR GO; GO:0030173; C-integral to Golgi membrane; IEA.
 DR GO; GO:0008373; F-sialyltransferase activity; IEA.
 DR GO; GO:0006486; P-protein amino acid glycosylation; IEA.
 DR InterPro; IPR001675; Glyco transferase; IEA.
 DR InterPro; IPR012163; Sialyl transferase; IEA.
 DR Pfam; PF00777; Glyco transferase; IEA.
 DR PIRSF; PIRSF005557; Sialyl transferase; IEA.
 KW Glycosyltransferase; Transferase
 SQ SEQUENCE 398 AA; 44836 MW; 48F58B82E4B69A26 CRC64;
 Query Match 84.3%; Score 1772; DB 2; Length 398;
 Best Local Similarity 82.7%; Pred. No. 2e-130;
 Matches 329; Conservative 30; Mismatches 39; Indels 0; Gaps 0;
 QY 1 MRSGGTLFALIGSLMLLLRLMPCADAPARSRLMEGSRDTSATKLTLMSPPTP 60
 DB 1 MRPGGALLALLALLLLLLRLMPCADAPGRARILVEESREATHGTPAALRTLRSPATA 60
 QY 61 VPRTRNSTYLDKTTQITEKCKDQYSLNSLNKTRRYSEDDYLOITITNIQRCPMNRQAE 120
 DB 61 VPRATNSTYLNKSLQITEKCKNQYIESFSNKTGYSNDYLOITIDQSCPWKQAE 120
 QY 121 EYDNFRKLASCDDAQDFVVSQNTPVGTNNMSYEVEKSHPIRENIHMFVPVSPFVD 180
 DB 121 EYANFRKLASCDDAQDFVVSQNTPVGTNNMSYEVEKSHPIRENIHMFVPVSPFVD 180
 QY 181 YPNQCAVVGNGGILNKSICGAEIDSDVFRCNLPPTTGSASKQVGSKTNLVTNPSII 240
 DB 181 YPNQCAVVGNGGILNKSICGTEIDSDVFRCNLPPTTGDVSKQVGSKTNLVTNPSII 240
 QY 241 TLKYONLKEKKAQFLEDISTYGDALFLLPAPSFYRANTGTSFKVYQTLKESKQKVLFFH 300
 DB 241 TLKYGNLKEKKAFLIEDIATYGDALFLLPAPSFYRANTGTSFKVYTLLESKARQKVLFFH 300
 QY 301 PRLRHALLFWRTKGTAVYRLSTGLMIASVAVELCNVLYGFWPFSKTIEDTFLSHHHY 360
 DB 301 PKYLDLALFWRTKGTAVYRLSTGLMITSVAVELCNVLYGFWPFSKTIEDTIPVSHHHY 360
 QY 361 DNKLPHGHQHPKQKYSQILQHLKMGKGLLKQFSKCEVA 398
 DB 361 DNKLPHGHQHPKQKYSQILQHLKMGKGLLKQFSKCEVA 398
 RESULT 7
 SIA8F PANTR
 ID SIA8F PANTR STANDARD; PR; 398 AA.
 AC P61648;
 DT 07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
 DT 07-JUN-2004, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE Alpha-2,8-sialyltransferase 8F (C 2.4.99.-) (ST8SIA VI).
 GN Name=ST8SIA6; Synonyms=SIAT8F;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pan.
 NCBI_TaxID=9598;
 [1]
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP Harduin-Lepers A., Martinez-Duncan I., Mollicone R., Delannoy P., Oriol R.;
 RT "Phylogeny of sialyltransferases";
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Prefers O-glycans to N-glycans or glycolipids as acceptor substrates. The minimal acceptor substrate is the NeuAc-alpha-2,3(6)-Gal sequence at the nonreducing end of their

CC carbohydrate groups (By similarity).
 CC -1- PATHWAY: Glycosylation.
 CC -1- SUBCELLULAR LOCATION: Golgi apparatus; Golgi membrane; single-pass
 CC type II membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the glycosyltransferase 29 family.
 CC
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 CC
 CC EMBL: AJ697663; CAC26901.1; -; mRNA.
 DR InterPro: IPR001675; Glyco trans_29.
 DR InterPro: IPR012163; Sialyl trans.
 DR Pfam: PF00777; Glyco trans_29; 1.
 DR PIRSF: PIRSF005557; Sialyl trans; 1.
 KW Glycoprotein; Glycosyltransferase; Golgi stack; Membrane;
 KW Signal-anchor; Transferase; Transmembrane
 FT CHAIN 1 398 Alpha-2,8-sialyltransferase 8F.
 FT /Ftrid-PRO_0000149301.
 FT TOPO_DOM 1 3 Cytoplasmic (Potential).
 FT TRANSMEM 4 24 Signal-anchor for type II membrane
 FT protein (Potential).
 FT TOPO_DOM 25 398 Luminal (Potential).
 FT CARBOHYD 66 66 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 196 196 N-linked (GlcNAc...) (Potential).
 FT DISULFID 186 335 By similarity.
 FT SEQUENCE 398 AA; 44859 MW; 45794C7A63425554 CRC64;

Query Match 83.9%; Score 1763; DB 1; Length 398;
 Best Local Similarity 82.2%; Pred. No. 1e-129;
 Matches 327; Conservative 31; Mismatches 40; Indels 0; Gaps 0;

QY 1 MRSGGTFALIGSIMLLMLLLMLLWCPADAPARSRLLMEGSRDTSAGTSAALKTLWSPPTP 60
 DB 1 MRSGGTFALIGSIMLLMLLLMLLWCPADAPARSRLLMEGSRDTSAGTSAALKTLWSPPTP 60
 QY 61 VPRTRNSTYLDKKTQITTEKCKDQYSLNSLNKTRYSDDYLLQTTNIQRCWPNRQAE 120
 DB 61 VPRATNSTYLNKSLHTECKNLQVIESFNKTKGYSNDYLLQITDIQSCPWKQAE 120
 QY 121 EYDNFRAKLASCDDAIQDFVVSQNTPTVGTNMSYEVEKHHIPIRENIFHMFVVSQPFVD 180
 DB 121 EYANFRAKLASCDDAVQNFVVSQNTPTVGTNMSYEVEKKEIPIKKNIFHMFVVSQPFVD 180
 QY 181 YPYNQCAVVGNGGILNKSICGAEIDKSDFFVRCNLPPTITGSASDKVSKTNLVTNPSII 240
 DB 181 YPYNQCAVVGNGGILNKSICGAEIDKSDFFVRCNLPPTITGSASDKVSKTNLVTNPSII 240
 QY 241 TLKYQNLKEKKAQFLEDISTYGDALLPAFSYRANTGISFKVYOTLKESKMRQKVLFFH 300
 DB 241 TLKYQNLKEKKAQFLEDIATYGEAFLLPAFSFRANTGTSGFKVYITLLESKARQKVLFFH 300
 QY 301 PRYLRLHALFWRTKGTAYRLSTGLMTASVAVELCNVKGWFPFSKTTEDTPLSHYY 360
 DB 301 PKYLKOLALFWRTKGTAYRLSTGLMTASVAVELCNVKGWFPFSKTTEDTPLSHYY 360
 QY 361 DNMLPKHGHQMPKEYSQMLQLHMRGILKIQFSKCEA 398
 DB 361 DNKLPRKHGHQMPKEYSQMLQLHMRGILKIQFSKCEA 398

RESULT 8

Q5NDG0 BOVIN PRELIMINARY; PRT; 398 AA.
 AC Q5NDG0
 DT 01-FEB-2005, integrated into UniProtKB/TrEMBL.
 DT 01-FEB-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Alpha-2,8-sialyltransferase (Fragment).
 GN Names: sial8F;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15843597; DOI=10.1093/glycob/cwi063;
 RA Harduin-Lepers A., Mollicone R., Delannoy P., Oriol R.;
 RT "The animal sialyltransferases and sialyltransferase-related genes: a
 RT phylogenetic approach.";
 RL Glycobiology 15:805-817 (2005).
 CC
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 CC
 CC EMBL: AJ868431; CA130813.1; -; mRNA.
 DR Ensembl: ENSBTAG00000011366; Bos taurus.
 DR GO: GO:0030173; C: integral to Golgi membrane; IEA.
 DR GO: GO:0008373; F: sialyltransferase activity; IEA.
 DR GO: GO:0006486; P: protein amino acid glycosylation; IEA.
 DR InterPro: IPR001675; Glyco trans_29.
 DR InterPro: IPR012163; Sialyl trans.
 DR Pfam: PF00777; Glyco trans_29; 1.
 DR PIRSF: PIRSF005557; Sialyl trans.
 KW Glycosyltransferase; Transferase
 FT NON_TER 1 1
 FT NON_TER 398 398
 FT SEQUENCE 398 AA; 45033 MW; 549EC59B50CCFD8 CRC64;

Query Match 76.0%; Score 1597; DB 2; Length 398;
 Best Local Similarity 74.6%; Pred. No. 1.e-116;
 Matches 297; Conservative 46; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRSGGTFALIGSIMLLMLLLMLLWCPADAPARSRLLMEGSRDTSAGTSAALKTLWSPPTP 60
 DB 1 MRSGGTFALIGSIMLLMLLLMLLWCPADAPARSRLLMEGSRDTSAGTSAALKTLWSPPTP 60
 QY 61 VPRTRNSTYLDKKTQITTEKCKDQYSLNSLNKTRYSDDYLLQTTNIQRCWPNRQAE 120
 DB 61 VPRATNSTYLNKSLHTECKNLQVIESFNKTKGYSNDYLLQITDIQSCPWKQAE 120
 QY 121 EYDNFRAKLASCDDAIQDFVVSQNTPTVGTNMSYEVEKHHIPIRENIFHMFVVSQPFVD 180
 DB 121 EYANFRAKLASCDDAVQNFVVSQNTPTVGTNMSYEVEKKEIPIKKNIFHMFVVSQPFVD 180
 QY 181 YPYNQCAVVGNGGILNKSICGAEIDKSDFFVRCNLPPTITGSASDKVSKTNLVTNPSII 240
 DB 181 YPYNQCAVVGNGGILNKSICGAEIDKSDFFVRCNLPPTITGSASDKVSKTNLVTNPSII 240
 QY 241 TLKYQNLKEKKAQFLEDISTYGDALLPAFSYRANTGISFKVYOTLKESKMRQKVLFFH 300
 DB 241 TLKYQNLKEKKAQFLEDIATYGEAFLLPAFSFRANTGTSGFKVYITLLESKARQKVLFFH 300
 QY 301 PRYLRLHALFWRTKGTAYRLSTGLMTASVAVELCNVKGWFPFSKTTEDTPLSHYY 360
 DB 301 PKYLKOLALFWRTKGTAYRLSTGLMTASVAVELCNVKGWFPFSKTTEDTPLSHYY 360
 QY 361 DNMLPKHGHQMPKEYSQMLQLHMRGILKIQFSKCEA 398
 DB 361 DNKLPRKHGHQMPKEYSQMLQLHMRGILKIQFSKCEA 398

RESULT 9

Q6ZXC6 CHICK PRELIMINARY; PRT; 398 AA.
 AC Q6ZXC6;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Alpha-2,8-sialyltransferase.
 GN Names: sial8F;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; C

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OC Gallus.
OK NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Harduin-Lepers A., Mollicone R., Delannoy P., Oriol R.;
RX PubMed=15843597; DOI=10.1093/glycob/cwi063;
RT "The animal sialyltransferases and sialyltransferase-related genes: a
RL phylogenetic approach.";
CC Glycobiology 15:805-817(2005).
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CC -----
DR EMBL; AJ699424; CAG27886.1; -, mRNA.
DR GO; GO:0030173; C: integral to Golgi membrane; IEA.
DR GO; GO:0008373; F: sialyltransferase activity; IEA.
DR GO; GO:0006486; P: protein amino acid glycosylation; IEA.
DR InterPro; IPR001675; Glyco trans.29.
DR InterPro; IPR012163; Sialyl trans.
DR Pfam; PF00777; Glyco trans.29; 1.
DR PIRSF; PIRSF005557; Sialyl trans; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 398 AA; 44877 MW; 7D334FF316460667 CRC64;

Query Match 56.3%; Score 1183; DB 2; Length 398;
Best Local Similarity 60.7%; Pred. No. 3.5e-84;
Matches 224; Conservative 49; Mismatches 90; Indels 6; Gaps 2;

QY 35 LLMEGSRD---TSGTSAALKTLSPPTVPTRNSTVLDK---TQTTEKCKDLOVSL 88
DB 29 LLARGWEEAEVATVPKVRALRSPLTSLQTEHRTANKDGIYQELDTCKCAIQDNI 88

QY 89 NLSNKTRRYSEDDYLOTITNIQRCPMNRQAEYDNFRAKLASCCDAIQDFVWSQNTPTV 148
DB 89 LSSSFKKKRYPDYLYHVKLQNCQTVWRPEESAKFRSELASCNAVHPIASQNTPL 148

QY 149 GTNMSYEVESKXKPIPIRENIHFMPVSPQFVDYFYNQCAVNGGILNKSCLGAEIDKSD 208
DB 149 GSNMSYEVDSKKTLLTIEDIFMLFVSPSLSPVFPKCAVNGGILNKSCLGAEIDRSD 208

QY 209 VFVRCNLPPTTGSADKVGSKTNLVNPSITILKYQNLKKAQFLEIDISTYGDALL 268
DB 209 VFVRCNLPPTTGSISKVGSKTNLVNPSITILKYQNLKKAQFLEIDISTYGDALL 268

QY 269 PAFSFRANTGISFKVYQTLKESKMRQVLPFPHPYRLHLALFWRTKGTAYRLSTGLMIA 328
DB 269 PAFSFRNTATSPKVVHTLQEFKATQRAIPFPHTYLNLAQFWRTKGVAYRLSSGFMIT 328

QY 329 SVAVELCNKLYGFWFPFSKTIEDTPLSHHYDNLMPKHGFHOMPKKEYSOMLQHLHMGIL 388
DB 329 SAAVELCNKLYGFWFPFSKTEKMPISHHYDNLMPKHGFHOMPKKEYNQILQHLHGKIK 388

QY 389 KLPQSKCET 397
DB 389 KLPQSKCES 397

RESULT 10
Q6KC02_BRARE PRELIMINARY; PRT; 343 AA.
AC Q6KC02;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Alpha-2,8-sialyltransferase ST8Sia V (EC 2.4.99.8) (Fragment).
GN Name=siat 8E;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
CC -----
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RX PubMed=15843597; DOI=10.1093/glycob/cwi063;
RA Harduin-Lepers A., Mollicone R., Delannoy P., Oriol R.;
RT "The animal sialyltransferases and sialyltransferase-related genes: a
RL phylogenetic approach.";
CC Glycobiology 15:805-817(2005).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AJ715546; CAG29385.1; -, mRNA.
DR GO; GO:0030173; C: integral to Golgi membrane; IEA.
DR GO; GO:0008373; F: alpha-N-acetylneuraminate alpha-2,8-sialylt. .; IEA.
DR GO; GO:0003828; P: protein amino acid glycosylation; IEA.
DR GO; GO:0006486; P: protein amino acid glycosylation; IEA.
DR InterPro; IPR001675; Glyco trans.29.
DR InterPro; IPR00777; Glyco trans.29.
KW Glycosyltransferase; Transferase.
FT NON_TER 1 343
FT NON_TER 343 343
SQ SEQUENCE 343 AA; 39768 MW; 2B686D818AC9136 CRC64;

Query Match 34.6%; Score 728; DB 2; Length 343;
Best Local Similarity 44.3%; Pred. No. 1.5e-48;
Matches 134; Conservative 56; Mismatches 113; Indels 0; Gaps 0;

QY 93 NKTRRYSEDDYLOTITNIQRCPMNRQAEYDNFRAKLASCCDAIQDFVWSQNTPTV 152
DB 40 NYIKRVKTSLEFRWRNLQVCKVQNKKEEDTNFMSLRCCNAPSFLLTKRNTPSGPKL 99

QY 153 SYEVESKXKPIPIRENIHFMPVSPQFVDYFYNQCAVNGGILNKSCLGAEIDKSDVFR 212
DB 100 RYEVDTSGILHISPEIFKMPFDDPFSKSFQKCAVNGGILNKSCLGAEIDKSDVFR 159

QY 213 CNLPPTTGSADKVGSKTNLVNPSITILKYQNLKKAQFLEIDISTYGDALLPAPS 272
DB 160 CNIPVPSDLYSQDVGSKTDLVTTPSIITERFQLEKWRKPFYEVLYQYENSVVLPAPY 219

QY 273 YRANTGISFKVYQTLKESKMRQVLPFPHPYRLHLALFWRTKGTAYRLSTGLMIASVAV 332
DB 220 NTRNTDVSFRKMLDDPFESSRGFFPHQYLLNVQRFVAVQGVRAKLSGLMLVTAAM 279

QY 333 ELCENVKLYGFWFPFSKTIEDTPLSHHYDNLMPKHGFHOMPKKEYSOMLQHLHMGILKQF 392
DB 280 ELCEVHLYGFWFPFNPSPGIPFHHYDNLMPKHGFHOMPKKEYSOMLQHLHMGILKQF 339

QY 393 SKC 395
DB 340 GPC 342

RESULT 11
Q6KC00_TETNG PRELIMINARY; PRT; 379 AA.
AC Q6KC00;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Alpha-2,8-sialyltransferase ST8Sia V (EC 2.4.99.8) (Fragment).
GN Name=siat 8E;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Ecomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15843597; DOI=10.1093/glycob/cwi063;
RA Harduin-Lepers A., Mollicone R., Delannoy P., Oriol R.;
RT "The animal sialyltransferases and sialyltransferase-related genes: a
RL phylogenetic approach.";
CC Glycobiology 15:805-817(2005).
CC -----
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DR Pfam; PF00777; Glyco transf 29; 1.
DR PRSP; PRS005557; Sialyl trans; 1.
KW Glycosyltransferase; Transferase.
FT NON TER 1 372 372
SQ SEQUENCE 372 AA; 42362 MW; 74842EC22385F239 CRC64;

Query Match 34.2%; Score 719.5; DB 2; Length 372;
Best Local Similarity 41.9%; Pred. No. 7.7e-48;
Matches 132; Conservative 61; Mismatches 121; Indels 1; Gaps 1;

QY 81 CKDQYSLNSLNKTRYSDDYQTITNORCPWNRQAEYDNFRKLAASCCDAIQDFV 140
Db 65 CRELRQIMDKVLT-MVKTSDLEFRWRNLQICRWBQNKETSFPKMSLRCCNAPSLF 123
QY 141 VSONTPVGTNMSYEVSCKKHIRENIFHMFVPSQFVDYPYNQCAVGVNGGILNLSLC 200
Db 124 TTKRNPAGTKLRYEVDTSGLITAEVFKMFPDDMPYSKQPKKCAVGVNGGIIKNSKC 183
QY 201 GAEDSKDFVRCNLPPITGSASDVGSKTNLVNPSIITLKYNLKEKKAQFLEDIST 260
Db 184 GKEIDSADFVRCNIPPISEKYSLVGSKTNLVNPSIITLKYNLKEKKAQFLEDIST 243
QY 261 YGDAFLLLPAPSYRANTGISFKYQTLKESQKQKVLFFHPRYLRLHALLFWRTKGVTAIR 320
Db 244 YENSAVLPAFYNTNTRDVSFRVYMLDDFDSQGVFFHFPQYLLNVQRFWAVQGVRAKR 303
QY 321 LSTGLMTASVAVELCENVKLYGEPFSKTIEDTPLSHHYDDNMLPKHGFHOMPKKEYSOML 380
Db 304 LSSGLMLVTAALWCCEVHLGYEAFPMNPSGIFITHHYDDNVKPRGPFHAMPHIEFNFI 363
QY 381 QLMHKGILKQFSKC 395
Db 364 HMTRGIVNVHTGQC 378

RESULT 14
Q6KC01_FUGRU PRELIMINARY; PRT; 379 AA.
ID Q6KC01_FUGRU PRELIMINARY; PRT; 379 AA.
AC Q6KC01_FUGRU PRELIMINARY; PRT; 379 AA.
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Alpha-2,8-sialyltransferase ST8Sia V (EC 2.4.99.8) (Fragment).
GN Name-siat 8E;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15843597; DOI=10.1093/glycob/cwi063;
RA Harduin-Lepers A., Mollicone R., Delannoy P., Oriol R.;
RT "The animal sialyltransferases and sialyltransferase-related genes: a
phylogenetic approach.";
RL Glycobiology 15:805-817(2005).
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EMBL; AJ715547; CAG29386.1; mRNA.
DR GO; GO:00030173; C:integral to Golgi membrane; IEA.
DR GO; GO:0003828; F:alpha-N-acetylneuraminic acid glycosylation; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001675; Glyco trans. 29.
DR Pfam; PF00777; Glyco transf 29; 1.
KW Glycosyltransferase; Transferase.
FT NON TER 1 379 379
SQ SEQUENCE 379 AA; 43847 MW; F4E16D8D37812860 CRC64;

Query Match 34.0%; Score 715.5; DB 2; Length 356;
Best Local Similarity 40.2%; Pred. No. 1.5e-47;
Matches 138; Conservative 64; Mismatches 116; Indels 25; Gaps 4;

QY 57 PTPVPRTRNSYLDKTKTITECKDQYSLNSLNKTRYSDDYQITITNORCPWNRQAEYDNFRKLAASCCDAIQDFV 140
Db 38 PASRIPOKASN-----TQSCPKDQSVIIGKALGN-----YNSN-----WK 73

Query Match 34.2%; Score 719.5; DB 2; Length 379;
Best Local Similarity 41.9%; Pred. No. 7.9e-48;
Matches 132; Conservative 61; Mismatches 121; Indels 1; Gaps 1;

QY 81 CKDQYSLNSLNKTRYSDDYQTITNORCPWNRQAEYDNFRKLAASCCDAIQDFV 140
Db 65 CRELRQIMDKVLT-MVKTSDLEFRWRNLQICRWBQNKETSFPKMSLRCCNAPSLF 123
QY 141 VSONTPVGTNMSYEVSCKKHIRENIFHMFVPSQFVDYPYNQCAVGVNGGILNLSLC 200
Db 124 TTKRNPAGTKLRYEVDTSGLITAEVFKMFPDDMPYSKQPKKCAVGVNGGIIKNSKC 183
QY 201 GAEDSKDFVRCNLPPITGSASDVGSKTNLVNPSIITLKYNLKEKKAQFLEDIST 260
Db 184 GKEIDSADFVRCNIPPISEKYSLVGSKTNLVNPSIITLKYNLKEKKAQFLEDIST 243
QY 261 YGDAFLLLPAPSYRANTGISFKYQTLKESQKQKVLFFHPRYLRLHALLFWRTKGVTAIR 320
Db 244 YENSAVLPAFYNTNTRDVSFRVYMLDDFDSQGVFFHFPQYLLNVQRFWAVQGVRAKR 303
QY 321 LSTGLMTASVAVELCENVKLYGEPFSKTIEDTPLSHHYDDNMLPKHGFHOMPKKEYSOML 380
Db 304 LSSGLMLVTAALWCCEVHLGYEAFPMNPSGIFITHHYDDNVKPRGPFHAMPHIEFNFI 363
QY 381 QLMHKGILKQFSKC 395
Db 364 HMTRGIVNVHTGQC 378

RESULT 15
Q6KBZ7_ERARE PRELIMINARY; PRT; 356 AA.
ID Q6KBZ7_ERARE PRELIMINARY; PRT; 356 AA.
AC Q6KBZ7_ERARE PRELIMINARY; PRT; 356 AA.
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Alpha-2,8-sialyltransferase ST8Sia VI (EC 2.4.99.8) (Fragment).
GN Name-siat 8F;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15843597; DOI=10.1093/glycob/cwi063;
RA Harduin-Lepers A., Mollicone R., Delannoy P., Oriol R.;
RT "The animal sialyltransferases and sialyltransferase-related genes: a
phylogenetic approach.";
RL Glycobiology 15:805-817(2005).
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EMBL; AJ715551; CAG29390.1; mRNA.
DR Ensembl; ENSDARG0000021195; Danio rerio.
DR GO; GO:00030173; C:integral to Golgi membrane; IEA.
DR GO; GO:0003828; F:alpha-N-acetylneuraminic acid glycosylation; IEA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
DR InterPro; IPR001675; Glyco trans. 29.
DR Pfam; PF00777; Glyco transf 29; 1.
KW Glycosyltransferase; Transferase.
FT NON TER 1 356 356
SQ SEQUENCE 356 AA; 40331 MW; 12228C77763558A CRC64;

Query Match 34.0%; Score 715.5; DB 2; Length 356;
Best Local Similarity 40.2%; Pred. No. 1.5e-47;
Matches 138; Conservative 64; Mismatches 116; Indels 25; Gaps 4;

QY 57 PTPVPRTRNSYLDKTKTITECKDQYSLNSLNKTRYSDDYQITITNORCPWNRQAEYDNFRKLAASCCDAIQDFV 140
Db 38 PASRIPOKASN-----TQSCPKDQSVIIGKALGN-----YNSN-----WK 73

Qy	117	ROAEYDNR	AKLASCCDAIQDFVUSONNTPVGTNMSYEVS	SKHPIPIRENIFHMFVSO	176
Db	74	KHEANYKFR	LLLNKCHAVSKAVVTQNTPLGSNVVYDGER	RKPLQVTQALYNILAKEQ	133
Qy	177	PFVDYPYNQ	CAVVGNGGIINKSLCGAEIDKSDVFRCNLP	PITGSASKDVGSKTNLVTN	236
Db	134	PFGNATWES	CAVVGNGSVLANSSCGEEINSAQFVIKCN	LPPLDDRYEKDVGNKTNLVTAN	193
Qy	237	PSIITLKYON	LKEKKAQFLEDISTYGDAPLLLPAPSYRANT	GISPKVYOTLKESQOROKV	296
Db	194	PSILHEKYS	GLMERRRPFVESLHSGQALLLPAPSYGHNT	PVSLRAFYTTLEDGCRDPLP	253
Qy	297	LFEPHPRYL	RHLALFWRTKGVTA	YRLSTGLMTASVAVELCENVKLYGFWPFSKTI	EDT-PL 355
Db	254	IFLNPYLR	KUTKFWREQGLNSVRPSTGLI	WASLALIEICTNVHLYGFWPFGKHPNDSRPI	313
Qy	356	SHHYDNNLP	KHGHQMPKEYSQMLQLHMRGILKQFSK	CETA	398
Db	314	TNHYDNR	ESKQNVHSMPEPEQLLKLHKQGVVHI	HLGECOPA	356

Search completed: May 26, 2006, 23:30:46
Job time : 306 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 26, 2006, 23:26:00 ; Search time 40 Seconds
(without alignments)
957.357 Million cell updates/sec

Title: US-10-501-930-1
 Perfect score: 2102
 Sequence: 1 MRSGGTFLAIGSLMLLLL.....MLQHRGILKLOPSKETA 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	702	33.4	342	2	JC5195	alpha-N-acetylneur	
2	701	33.3	359	2	JC4973	GM3 alpha-2,8-sial	
3	700	33.3	356	2	A54032	alpha-N-acetylneur	
4	677	32.2	376	2	JC5600	alpha-N-acetylneur	
5	474	22.5	380	2	JC6321	CMP-NeuAc-GM3 alph	
6	470	22.4	380	2	A56950	alpha-2,8-sialyltra	
7	419.5	20.0	359	2	S52425	polysialyltransfer	
8	418.5	19.9	359	2	JC4224	alpha-N-acetylneur	
9	416.5	19.8	359	2	IS3403	alpha-2,8-polysial	
10	408.5	19.4	375	2	I39169	sialyltransferase	
11	403.5	19.2	375	2	A46727	sialyltransferase	
12	395.5	18.8	375	2	I48686	N-glycan alpha 2,8	
13	352.5	16.8	322	2	B54898	STX protein - huma	
14	218.5	10.4	566	2	A49880	alpha-N-acetyl gala	
15	212	10.1	526	2	JC7248	alpha-N-acetyl gala	
16	208.5	9.9	342	2	S55675	Gal beta-1,3GalNac	
17	199.5	9.5	343	2	A54073	Gal beta-1,3GalNac	
18	196	9.3	337	2	S36824	beta-galactoside a	
19	191.5	9.1	340	2	IS4229	beta-galactoside a	
20	188.5	9.0	404	2	A54871	Gal beta-1, 3GalNA	
21	180.5	8.6	350	2	B54420	beta-galactoside a	
22	171.5	8.2	413	2	A41114	Gal beta 1,4 GlcNA	
23	170.5	8.1	329	2	A48715	gal-beta(1-3/1-4)G	
24	170.5	8.1	350	2	JC5251	beta-galactoside a	
25	169	8.0	350	2	A54420	beta-galactoside a	
26	166	7.9	406	2	A41734	beta-galactoside a	
27	165.5	7.9	332	2	A49879	alpha-2,3-sialyltr	
28	164	7.8	524	2	JC8017	beta-galactoside a	
29	160	7.6	398	2	G63216	protein T23G18.14	

LIGNMENTS

RESULT 1

JC5195
 alpha-N-acetylneuraminate alpha-2,8-sialyltransferase (EC 2.4.99.8) - rat
 N:AlphaAlternate names: GD3 synthase
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 05-Oct-2004
 C:Accession: JC5195
 R:Watanabe, Y.; Nara, K.; Takahashi, H.; Nagai, Y.; Sanai, Y.
 J. Biochem. 120, 1020-1027, 1996
 A:Title: The molecular cloning and expression of alpha2,8-sialyltransferase
 A:Reference number: JC5195; MUID:97137534; PMID:8982871
 A:Contents: brain
 A:Accession: JC5195
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-342 <WAT>
 A:Cross-references: UNIPROT:P70554; UNIPARC:UPI0000167AA8; DDBJ:D45255; NID
 C:Comment: This enzyme is responsible for the ganglioside pattern in tissue
 C:Superfamily: sialyltransferase
 C:Keywords: glycoprotein; glycosyltransferase
 F:13-34/Domain: transmembrane #status predicted <TMM>
 F:120-168/Region: sialyl motif
 F:258-280/Region: sialyl motif
 F:56-104, 199, 230/binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	33.4%;	Score	702;	DB	2;	Length	342;
Best Local Similarity	43.0%;	Prod.	No. 1.5e-48;				
Matches	128;	Conservative	65;	Mismatches	103;	Indels	2;
Gaps	2;						

QY	99	SEDDYLOTITNORCPWNRQAEVNDNFRAKLASCDDAIQDFVVSQNNTPVGTNMSYEVES	158
DB	38	NKEIIVQGVLAQRTAWRNRQTAARLFRRQMBECCPAHLFAMTKVNSPMGKSLWYDGEF	96
QY	159	KKHIPIRENIFMFVPVSQPFVDTPYNQCAVVGNGGILINKSLCGAIEDKSDVFPRCNLPPI	218
DB	97	LYSLTIDNSTYSLFPQATPPQSLPCKCAVVGNGGILKMSGCGRQIDEANFVMRCNLPPL	155
QY	219	TSGASKDVGSKTNLVTVPNSITLKYONLKEKAAQFLEDISTYGDAPFLLLPAPSYRANTG	278
DB	156	SSEYTRDVGSKTQLVTANPSITLDFENLLWSRKKCFVDNNKIYNHYSIYNPAPSMKTGTE	215
QY	279	ISFKVYOTLKBKSMRKVLFFHRSYLRHLALFWRTKGVTAURLSTGLMIASVAVELCENV	338
DB	216	PSLRVYIYLLKAGANTVLFAHNFLENRTGKFWKGRIHAKRLSTGLFLVSAALGLCEEV	275
QY	339	KLYGFWPPFKTIEDTPLSHHYTNMLPKGHFHQMPKEYSQMLQHRMGIKLKLFQSKCE	396
DB	276	SIYGFWFPFVNNQGEPISSHYYTNVLPFSGFHAMPEEFLQLWYLHKMGALRMQLDPCE	333

RESULT	2
JC4973	

GM3 alpha-2,8-sialyltransferase (EC 2.4.99.-) - rat

N/Alternate names: GD3 synthase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 05-Oct-2004
C/Accession: J04973
R/Zeng, G.; Gao, L.; Ariga, T.; Yu, R.K.
Biochem. Biophys. Res. Commun. 226, 319-323, 1996
A/Title: Molecular cloning of cDNA for rat brain GD3-synthase.
A/Reference number: J04973; MUID:96400257; PMID:18066633
A/Accession: J04973
A/Molecule type: mRNA
A/Residues: 1-359 <ZEN>
A/Cross-references: UNIPROT:P70554; UNIPARC:UPI000000E8795; GB:U53883; NID:G1628556; PID:
A/Experimental source: Brain
C/Comment: This enzyme is a key branching-point enzyme which regulates the synthesis of
C/Superfamily: sialyltransferase
C/Keywords: glycosyltransferase

Query Match 33.3%; Score 701; DB 2; Length 359;
Best Local Similarity 43.0%; Pred. No. 1.9e-48;
Matches 128; Conservative 65; Mismatches 103; Indels 2; Gaps 2;

QY 99 SEDYLQTIINICRCPNQAEEYDNFRKLASCDAIQDFVVSQNTTPTVGTNMSYEVS 158
DB 52 NKEIVGVGL-AQRTAWRRNQTSARLFRKQEDCCNPAHLFAMTKVNSPMGKSLWDGEF 110
QY 159 KXHIPIRENTFHMPPVSPQFVDYVPYNQCAVVGNGILNKLSCGAEIDKSDVFRCNLPPI 218
DB 111 LYSITIDTSYSLFPQATPF-QLPKKCAVVGNGILKMSGCGRQIDEANFVRCNLPL 169
QY 219 TGSASKDVGSKTNLVTVNPSIITIKYONLKEKKAQFLEDISTYGDAPLLLPAPSYRANTG 278
DB 170 SSEYTRDVGSKTQLVANTPSIIRQRFENLWSRCKFVDNMKNIYNSHYINPAFPMKGTGE 229
QY 279 ISFVYQYTLKESKMRQKVLFFHRYLRHLALFWRTKGVATYRLSTGLMIASVAVELCENV 338
DB 230 PSURVYITLKDAGNQVTLFANPFLRNIGKFWKRGIHAKRLSTGLFVSAALGLCEEV 289
QY 339 KLYGFWFPSFTIEDTPLSHSYDYNMLPKHGFHQMKPEYSQMLQHLMRGILKLOFSKCE 396
DB 290 SIYGFWFPSVNMQGEPISSHYYDNLVFPFSGFHAMPEEFQLWLWHLKMGALRMQLDPCE 347

RESULT 3
A54032
alpha-N-acetylneuraminate alpha-2,8-sialyltransferase (EC 2.4.99.8) - human
N/Alternate names: G-D3 synthase; G-m3-specific alpha-2,8-sialyltransferase; gangliosidase
C/Species: Homo sapiens (man)
C/Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 05-Oct-2004
C/Accession: A54032; K39330; J59317
R/Sasaki, K.; Kurata, K.; Kojima, N.; Kurosawa, N.; Ohta, S.; Hanai, N.; Tsuji, S.; Nishij. Biol. Chem. 269, 15950-15956, 1994
A/Title: Expression cloning of a G-M3-specific alpha-2,8-sialyltransferase (G-D3 synthase)
A/Reference number: A54032; MUID:94253194; PMID:8195250
A/Accession: A54032
A/Molecule type: mRNA
A/Residues: 1-356 <SAS>
A/Cross-references: UNIPROT:Q92185; UNIPARC:UPI000013596F; GB:X77922; NID:G510987; PID:
R/Haraguchi, M.; Yamashiro, S.; Yamamoto, A.; Furukawa, K.; Takamiya, K.; Lloyd, K.O.; S
Proc. Natl. Acad. Sci. U.S.A. 91, 10455-10459, 1994
A/Title: Isolation of GD3 synthase gene by expression cloning of GM3 alpha-2,8-sialyltra
A/Reference number: I39330; MUID:95024133; PMID:7937974
A/Accession: I39330
A/Molecule type: mRNA
A/Residues: 16-356 <RES>
A/Cross-references: UNIPARC:UPI00001576C8; GB:L32867; NID:G662253; PID:AAA62366.1; PID:
R/Nara, K.; Watanabe, Y.; Maruyama, K.; Kasahara, K.; Nagai, Y.; Sanai, Y.
Proc. Natl. Acad. Sci. U.S.A. 91, 7952-7956, 1994
A/Title: Expression cloning of a CMP-NeuAc:NeuAc alpha2-3Gal beta1-4Glc beta1-1' Cer alp
A/Reference number: I59317; MUID:94336665; PMID:8058740
A/Accession: I59317
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA

C;Keywords: transmembrane protein

Query Match 22.4%; Score 470; DB 2; Length 380;
Best Local Similarity 33.1%; Pred. No. 6.6e-30;
Matches 113; Conservative 58; Mismatches 128; Indels 42; Gaps 10;

QY 69 YLDSEKTVITKCKDLQVLSNFKTRRYSEDYLOTTINIQRCP--WNRQAEEYDNPFR 126
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB 67 FLDSQFVPIT-----NSRTH-----LQEKPSKWTFNRTAFLHOR 101
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 127 AKLASCCDAIQDFVVSONNTPVGTNNMSEVESKKHI-PIRENIHFMPVPVSOPFDVDYPNO 185
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB 102 QEILQHVDVINRKSTKSVRICQLMHYDYSSHKYVFISINNFRSLLPDDVSPIMNKRYNV 161
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 186 CAVVGNGGILNKSLCGASIDKSEIYFRCNLPPITGSASKDVSGSKTNLTVTNPSIITLKYYQ 245
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB 162 CAVVGNIGILAGSQCGQEIDKSIIVSRCNFAP-TEAFHKDVGKTKNLTTFNFSILEKYVN 220
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 246 NLK--EKKAQPLEDISTGDAPFLPAFSYRANTGISPKYQTILKESKMRQKVLFPH-R 302
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB 221 NLLTIQRNNFFLSLKCLDGAILIPAFFHTSATVRTTLVDFFVEHGGQLVKQLAWPGN 280
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 303 YLRHLAFPWRKGVTAVALSTGLIASVAVELCENVKLYGFWPFS---KTIEDTPLSHHY 359
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB 281 IMQHVNYRWKNKHUSPKKLSTGLMYTLASAICEEHLYGFWFPGPDNTREDLP--VHY 338
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 360 YDNMLPK-----HGPHOMPKEYSOMQLHMKGILKLQFSKC 395
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB 339 YDKGTRFTWKQESHQLPAEFQLLYRMHGEGLTKLTLSHC 379
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

RESULT 7
S52425
polysialyltransferase-1 - Chinese hamster
C;Species: Cricetus griseus (Chinese hamster)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004
C;Accession: S52425
R;Eckhardt, M.; Muehlenhoff, M.; Bethe, A.; Koopman, J.; Froesch, M.; Gerardy-Schahn, R.
Nature 373, 715-718, 1995
A;Title: Molecular characterization of eukaryotic polysialyltransferase-1.
A;Reference number: S52425; MUID:95157675; PMID:7854457
A;Accession: S52425
A>Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-359 <ECK>
A;Cross-references: UNIPROT:Q64690; UNIPARC:UPI000011D7F8; GB:Z46801; NID:g735953; PIDN:
C;Superfamily: sialyltransferase

Query Match 20.0%; Score 419.5; DB 2; Length 359;
Best Local Similarity 28.9%; Pred. No. 6.7e-26;
Matches 107; Conservative 78; Mismatches 160; Indels 25; Gaps 9;

QY 37 MEGSRDTSGTSAALKTLWSPTTPVPRTNSTYLDEKTKOIT---EKKCLQYSINSLSN 93
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB 1 MRSIRKRWITICTISILLIFKYTKETARTE-----EQHOTLIGDELCL--LSRSLVNSSD 53
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 94 KTRYSEDYLOTTINIQRCPMWKOAEEDYNFRKLASCDDAIQDFVVSONNTPVGTNNMS 153
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB 54 KIIRKASTIFQ--HSVQ--GHFNSSLVLEIKRNILFLDAERDVSVKSSFKPGDVIH 109
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 154 YEYESKKHIPIRENIHFMPVSQFVDYPNQCAVVGNGGILNKSLCGAIEIDKSDFVPRC 213
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB 110 YVLDRRTLNISHDLHSLLPVSWKNRFKTCVAVVGNISGILLSDGCGKEIDSFNVFIRC 169
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 214 NLPIITGSASKDVSGSKTNLTVTNPSIIITLKYNLKEK--KAQFLEDISTYGDAFLLLPAF 271
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB 170 NLAEVVEFAA--DVGTGKSDFITNPSVVOQAFGGFRNESRAKFVHRSLMNDLSVLMIWIPAF 228
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 272 SYRANTGISFPKYOTLKESKMKRQKLVLFHPRYRLHALFWRTKGVTAVALSTGLMIASVA 331
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB 229 MVKGEKHEVWNALINKKLVATAYPSLRLIHAVRGWLTKNPKIKRPSTGLLMYTILA 288
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 332 VELCENVKLYGFWPFSKTIETEASHYYDNNMLPKHGF-----HMQPKYSQMQLHMR 385
||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

RESULT 9
 159403
 alpha-2,8-polysialyltransferase - human
 C/Species: Homo sapiens (man)
 C/Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 05-Oct-2004
 C/Accession: 159403
 R/Nakayama, J.; Fukuda, M.N.; Predette, B.; Ranscht, B.; Fukuda, M.
 Proc. Natl. Acad. Sci. U.S.A. 92, 7031-7035, 1995
 A:Title: Expression cloning of a human polysialyltransferase that forms the polysialylated

[illegible]

RESULT 15
JC7248
alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase (EC 2.4.99.3) I - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C:Accession: JC7248
R:Kurosawa, N.; Takashima, S.; Kono, M.; Ikehara, Y.; Inoue, M.; Tachida, Y.; Narimatsu, J. R. Biochem. 127, 845-854, 2000
A:Title: Molecular cloning and genomic analysis of mouse GalNAc alpha2,6-sialyltransferase
A:Reference number: JC7248
A:Accession: JC7248
A:Molecule type: mRNA
A:Residues: 1-526 <KUR>
A:Cross-references: UNIPARC:UPI00017C623; GB:Y11274
A:Experimental source: submaxillary gland
C:Comment: This enzyme, a transmembrane protein, is a key enzyme for O-linked oligosacch
thesizes cancer-associated carbohydrate antigen and shows acceptor substrate specificity
C:Genetics:
A:Gene: ST6GalNAC 1
A:Interons: 39/2: 262/1: 319/2: 365/3: 400/2: 430/2: 463/3

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 26, 2006, 23:22:10 ; Search time 197 Seconds
(without alignments)
923.716 Million cell updates/sec

Title: US-10-501-930-1

Perfect score: 2102

Sequence: 1 MRSQTLFALIGSLMLLLL.....MLQLHMRGILKIQSKCETA 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A Geneseq 8:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2102	100.0	398	7	ADC73011 Murine ST
2	1768	84.1	398	7	ADC73013 Human ST8
3	1180	56.1	247	4	AAG66954 Human sia
4	1180	56.1	247	8	ADV69201 Human cel
5	701	33.3	359	7	AD56214 Rat Prote
6	700	33.3	341	2	AA88326 Human alp
7	700	33.3	356	2	AA63225 Human alp
8	697	33.2	356	4	AA86207 Human GD3
9	477.5	22.7	380	7	ADD48076 Human Pro
10	474	22.5	380	7	ADD48074 Rat Prote
11	470	22.4	339	2	AAW05301 Extracell
12	470	22.4	380	5	AB57203 Mouse isc
13	470	22.4	381	2	AAW05300 Sia alpha
14	419.5	20.0	359	2	AA97868 Hamster p
15	418.5	19.9	359	7	AD660174 Rat Prote
16	416.5	19.8	359	7	AD660176 Human Pro
17	416.5	19.8	359	7	ADD48964 Human Pro
18	416.5	19.8	359	9	ADD48172 Human Pro
19	416.5	19.8	359	9	ADX57715 Rheumatol
20	416.5	19.8	359	9	ADY15754 PRO polyp
21	403.5	19.2	375	2	AA48342 Rat slaly
22	399.5	19.0	353	7	ADD48962 Rat Prote
23	399.5	19.0	353	7	ADD48170 Rat Prote

24	399.5	19.0	375	2	AA85241	Rat STX 8
25	346.5	16.5	222	2	AA85245	Human STX
26	290.5	13.8	273	7	ABR2846	Human car
27	272	12.9	122	4	AAG4710	Human col
28	224	10.7	50	5	ABP4610	Human ORF
29	221	10.5	328	10	AE86158	Human del
30	221	10.5	343	10	AE86090	Human del
31	221	10.5	368	10	AE86157	Human del
32	221	10.5	430	10	AE86156	Human del
33	221	10.5	468	4	AA83855	Amino aci
34	221	10.5	468	10	AE86155	Human del
35	221	10.5	476	10	AE86088	Human del
36	221	10.5	491	10	AE86154	Human del
37	221	10.5	522	4	AA83857	Amino aci
38	221	10.5	528	10	AE86153	Human del
39	221	10.5	565	10	AE86086	Human del
40	221	10.5	600	3	AA85733	Membrane-
41	221	10.5	600	3	AA85065	Human PRO
42	221	10.5	600	4	AA83856	Amino aci
43	221	10.5	600	4	AAU2402	Human PRO
44	221	10.5	600	4	AA85523	Human tra
45	221	10.5	600	4	AA85256	Human PRO

ALIGNMENTS

RESULT 1
ADC73011
ID ADC73011 standard; protein; 398 AA.
XX
AC ADC73011;
XX
DT 01-JAN-2004 (first entry)
XX
DE Murine ST8Sia VI protein.
XX
KW O-glycan alpha2,8-sialyltransferase;
KW beta-galactoside alpha2,6-sialyltransferase; cytotstatic; virucide;
KW antiinflammatory; neuroprotective; cancer metastasis; viral infection;
KW inflammation; nerve tissue; murine; mouse; ST8Sia VI; enzyme.
XX
OS Mus sp.
XX
FN WO2003064655-A1.
XX
PD 07-AUG-2003.
XX
PF 30-JAN-2003; 2003WO-JP000883.
XX
PR 30-JAN-2002; 2002JP-00021159.
XX
PR 24-APR-2002; 2002JP-00122673.
XX
PA (RIKE) RIKEN KK.
XX
PI Takashima S, Tsujimoto M, Tsui S;
XX
XX WPI; 2003-627613/59.
XX
DR N-PSDB; ADC73012.
XX
PT Sugar-chain synthases which are sialyltransferases and encoded genes,
PT applicable in drugs for inhibiting cancer metastasis, preventing viral
PT infection, inhibiting inflammation and potentiating nerve tissues.
XX
XX Claim 2; SEQ ID NO 1; 97pp; Japanese.
XX
CC The invention relates to a novel O-glycan alpha2,8-sialyltransferase
CC having a novel substrate specificity and selectivity and a novel beta-
CC galactoside alpha2,6-sialyltransferase having a novel substrate
CC specificity and selectivity. The enzymes of the invention demonstrate
CC cytotstatic, virucide, antiinflammatory and neuroprotective activities and
CC may be applicable in drugs for inhibiting cancer metastasis, preventing
CC viral infection, inhibiting inflammation and potentiating nerve tissues.

CC The current sequence is that of the murine ST8Sia VI protein of the
CC invention.
XX
SQ Sequence 398 AA;
Query Match 100.0%; Score 2102; DB 7; Length 398;
Best Local Similarity 100.0%; Pred. No. 2e-200;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRSGGTLFALIGSLMLLLMLCPADAPARSRLMEGSRDTSCTSAALKTLWSPPTP 60
Db 1 MRSGGTLFALIGSLMLLLMLCPADAPARSRLMEGSRDTSCTSAALKTLWSPPTP 60
Qy 61 VPRTRNSTYLDKKTQITEKCKDLOYSLSNKTTRYSEDDYLOTTINIORCPWNRQAE 120
Db 61 VPRTRNSTYLDKKTQITEKCKDLOYSLSNKTTRYSEDDYLOTTINIORCPWNRQAE 120
Qy 121 EYDNFRKLASCDAIQDFVVSQNTPTVGTNMSYEVSKEKHIPIRENIFHMFVPSQPPVD 180
Db 121 EYDNFRKLASCDAIQDFVVSQNTPTVGTNMSYEVSKEKHIPIRENIFHMFVPSQPPVD 180
Qy 181 YPNQCAVWGNGGILNKSLOCAGIDKSDVFRCNLPITGSASKDVGSKTNLVTNPSII 240
Db 181 YPNQCAVWGNGGILNKSLOCAGIDKSDVFRCNLPITGSASKDVGSKTNLVTNPSII 240
Qy 241 TLKYNLKEKKAQFLEDISTYGDAPFLLLPAPSYRANTGISFKVYQTLKESKORQKVLFFH 300
Db 241 TLKYNLKEKKAQFLEDISTYGDAPFLLLPAPSYRANTGISFKVYQTLKESKORQKVLFFH 300
Qy 301 PRYLRLHALFWRTKGVTAIRLSTGLMTASVAVELCENVKLYGFWPFSEKTIETDPLSHHY 360
Db 301 PRYLRLHALFWRTKGVTAIRLSTGLMTASVAVELCENVKLYGFWPFSEKTIETDPLSHHY 360
Qy 361 DNMLPKHGFHQPMPKEYSQMLQLHMRGILKLOFSKCEA 398
Db 361 DNMLPKHGFHQPMPKEYSQMLQLHMRGILKLOFSKCEA 398
RESULT 2
ADCT73013
ID ADCT73013 standard; protein; 398 AA.
XX
AC ADCT73013;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human ST8Sia VI protein.
XX
KW O-glycan alpha2,8-sialyltransferase;
KW beta-galactoside alpha2,6-sialyltransferase; cytostatic; virucide;
KW antiinflammatory; neuroprotective; cancer metastasis; viral infection;
KW inflammation; nerve tissue; human; ST8Sia VI; enzyme.
XX
OS Homo sapiens.
XX
FN WO2003064655-A1.
XX
PD 07-AUG-2003.
XX
XX 30-JAN-2003; 2003WO-JP000883.
XX
PR 30-JAN-2002; 2002JP-00021159.
PR 24-APR-2002; 2002JP-00122673.
XX
XX (RIKE) RIKEN KK.
XX
PI Takashima S, Tsujimoto M, Tsuji S;
XX
DR WPI; 2003-627613/59.
DR N-PSDB; ADCT73014.
XX
XX Sugar-chain synthases which are sialyltransferases and encoded genes,
XX applicable in drugs for inhibiting cancer metastasis, preventing viral

PT infection, inhibiting inflammation and potentiating nerve tissues.
XX
PS Claim 2; SEQ ID NO 3; 97pp; Japanese.
XX
CC The invention relates to a novel O-glycan alpha2,8-sialyltransferase
CC having a novel substrate specificity and selectivity and a novel beta-
CC galactoside alpha2,6-sialyltransferase having a novel substrate
CC specificity and selectivity. The enzymes of the invention demonstrate
CC cytostatic, virucide, antiinflammatory and neuroprotective activities and
CC may be applicable in drugs for inhibiting cancer metastasis, preventing
CC -viral infection, inhibiting inflammation and potentiating nerve tissues.
CC The current sequence is that of the human ST8Sia VI protein of the
CC invention.
XX
SQ Sequence 398 AA;
Query Match 84.1%; Score 1768; DB 7; Length 398;
Best Local Similarity 82.4%; Pred. No. 4.3e-167;
Matches 328; Conservative 30; Mismatches 40; Indels 0; Gaps 0;
Qy 1 MRSGGTLFALIGSLMLLLMLCPADAPARSRLMEGSRDTSCTSAALKTLWSPPTP 60
Db 1 MRSGGTLFALIGSLMLLLMLCPADAPARSRLMEGSRDTSCTSAALKTLWSPPTP 60
Qy 61 VPRTRNSTYLDKKTQITEKCKDLOYSLSNKTTRYSEDDYLOTTINIORCPWNRQAE 120
Db 61 VPRTRNSTYLDKKTQITEKCKDLOYSLSNKTTRYSEDDYLOTTINIORCPWNRQAE 120
Qy 121 EYDNFRKLASCDAIQDFVVSQNTPTVGTNMSYEVSKEKHIPIRENIFHMFVPSQPPVD 180
Db 121 EYDNFRKLASCDAIQDFVVSQNTPTVGTNMSYEVSKEKHIPIRENIFHMFVPSQPPVD 180
Qy 181 YPNQCAVWGNGGILNKSLOCAGIDKSDVFRCNLPITGSASKDVGSKTNLVTNPSII 240
Db 181 YPNQCAVWGNGGILNKSLOCAGIDKSDVFRCNLPITGSASKDVGSKTNLVTNPSII 240
Qy 241 TLKYNLKEKKAQFLEDISTYGDAPFLLLPAPSYRANTGISFKVYQTLKESKORQKVLFFH 300
Db 241 TLKYNLKEKKAQFLEDISTYGDAPFLLLPAPSYRANTGISFKVYQTLKESKORQKVLFFH 300
Qy 301 PRYLRLHALFWRTKGVTAIRLSTGLMTASVAVELCENVKLYGFWPFSEKTIETDPLSHHY 360
Db 301 PRYLRLHALFWRTKGVTAIRLSTGLMTASVAVELCENVKLYGFWPFSEKTIETDPLSHHY 360
Qy 361 DNMLPKHGFHQPMPKEYSQMLQLHMRGILKLOFSKCEA 398
Db 361 DNMLPKHGFHQPMPKEYSQMLQLHMRGILKLOFSKCEA 398
RESULT 3
AAG66954
ID AAG66954 standard; protein; 247 AA.
XX
AC AAG66954;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human sialic transferase 27 polypeptide.
XX
KW Human, sialic transferase 27; cancer; cytostatic; immunological disease;
KW human immunodeficiency virus; HIV; infection; inflammatory disease.
XX
OS Homo sapiens.
XX
FN CN1298005-A.
XX
PD 06-JUN-2001.
XX
PF 29-NOV-1999; 99CN-00124142.
XX
PR 29-NOV-1999; 99CN-00124142.
XX
PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.

XX Mao Y, Xie Y, Qiu M;
PI N-PSDB; AAH77592.
DR WPI; 2001-489682/54.
DR N-PSDB; AAH77592.
XX Human sialic transferase 27 as one new kind of polypeptide and
PT polynucleotides encoding this polypeptide.
XX Claim 1; Page 22-23 (disclosure); 29pp; Chinese.
XX The invention relates to a novel polypeptide, human sialic transferase
CC 27, polynucleotides encoding this polypeptide and a DNA recombination
CC process to produce the polypeptide. The polypeptide is useful for
CC treating various diseases, such as malignant tumors, nosohaemia, HIV
CC infection, immunological diseases and inflammatory diseases. The
CC invention also provides an antibody directed against the polypeptide. The
CC present sequence is the polypeptide of the invention.
XX Sequence 247 AA;
SQ

Query Match 56.1%; Score 1180; DB 4; Length 247;
Best Local Similarity 88.3%; Pred. No. 1e-108;
Matches 218; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
QY 152 MSYEVESSKGIPIRENIHFHMFVPSQFVDYPYNOCAVVGNGGILNKLSCGAEIDKSDVF 211
Db 1 MSYEVESSKGIPIKNIHFHMFVPSQFVDYPYNOCAVVGNGGILNKLSCGTEIDKSDVF 60
QY 212 RCNLPPTTGSASKDVSGKTNLVTNPSIITLKYNLKEKKAQFLEDISTYGDALLPAP 271
Db 61 RCNLPPTTGDVSKDVSGKTNLVTNPSIITLKYNLKEKKAQFLEDIATYGDALLPAP 120
QY 272 SYRANTGTSFKVYQTLKESKMRQKLVFFHPRYLRHLALFWRTKGVTVAYRLSTGLMIASVA 331
Db 121 SPRANTGTSFKVYTYLEESKARQKLVFFHPKYLKDLALFWRTKGVTVAYRLSTGLMITSVA 180
QY 332 VELCENVKLYGFWPFSKTIETPLSHHYDNNMLPKHGHPMPKEYSQMLQLHMRGILKLO 391
Db 181 VELCKNVKLYGFWPFSKTVEDIPVSHHYDNNMLPKHGHPMPKEYSQILQLHMKGILKLO 240
QY 392 FSKCETA 398
Db 241 FSKCEVA 247

RESULT 4
ADV69201
ID ADV69201 standard; protein; 247 AA.
XX AC ADV69201;
XX DT 24-FEB-2005 (first entry)
XX DE Human cell division regulating protein 27 SEQ ID NO 2.
XX cell division regulating protein 27; cancer; cytostatic; HIV infection;
XX anti-HIV; immune disorder.
XX Homo sapiens.
XX CN1493590-A.
XX PD 05-MAY-2004.
XX PF 30-OCT-2002; 2002CN-00137726.
XX PR 30-OCT-2002; 2002CN-00137726.
XX PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX PI Mao Y, Xie Y;

DR WPI; 2004-500615/48.
DR N-PSDB; ADV69200.
XX New polypeptide-human cell disintegrate regulatory protein 27 for
PT treating cancer, human immunodeficiency virus infection, and immunopathy.
XX Claim 1; SEQ ID NO 2; 25pp; Chinese.
XX The invention relates to human cell division regulating protein 27, the
CC polynucleotide encoding it, preparing the polypeptide by DNA recombination
CC techniques, application of the polypeptide in treating diseases, such as
CC cancer, human immunodeficiency virus (HIV) infection, immunopathy and the
CC antagonist of the polypeptide and its medical action and application of
CC the polynucleotide. The present sequence is that of the human cell
CC division regulating protein 27 of the invention.
XX Sequence 247 AA;
SQ

Query Match 56.1%; Score 1180; DB 8; Length 247;
Best Local Similarity 88.3%; Pred. No. 1e-108;
Matches 218; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
QY 152 MSYEVESSKGIPIRENIHFHMFVPSQFVDYPYNOCAVVGNGGILNKLSCGAEIDKSDVF 211
Db 1 MSYEVESSKGIPIKNIHFHMFVPSQFVDYPYNOCAVVGNGGILNKLSCGTEIDKSDVF 60
QY 212 RCNLPPTTGSASKDVSGKTNLVTNPSIITLKYNLKEKKAQFLEDISTYGDALLPAP 271
Db 61 RCNLPPTTGDVSKDVSGKTNLVTNPSIITLKYNLKEKKAQFLEDIATYGDALLPAP 120
QY 272 SYRANTGTSFKVYQTLKESKMRQKLVFFHPRYLRHLALFWRTKGVTVAYRLSTGLMIASVA 331
Db 121 SPRANTGTSFKVYTYLEESKARQKLVFFHPKYLKDLALFWRTKGVTVAYRLSTGLMITSVA 180
QY 332 VELCENVKLYGFWPFSKTIETPLSHHYDNNMLPKHGHPMPKEYSQMLQLHMRGILKLO 391
Db 181 VELCKNVKLYGFWPFSKTVEDIPVSHHYDNNMLPKHGHPMPKEYSQILQLHMKGILKLO 240
QY 392 FSKCETA 398
Db 241 FSKCEVA 247

RESULT 5
ADE56214
ID ADE56214 standard; protein; 359 AA.
XX AC ADE56214;
XX DT 29-JAN-2004 (first entry)
XX DE Rat Protein BAA08213, SEQ ID NO 2066.
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CC; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;

DT 26-JUN-1995 (first entry)
 DE Human alpha-2,8-sialyltransferase protein.
 XX
 KW Human; alpha-2,8-sialyltransferase; sialyltransferase; melanoma; E.coli;
 KW pUC119; expression vector; pAMOPRC3Sc; PCR; amplify; primer; sugar chain;
 KW physiological; ganglioside.
 XX
 OS Homo sapiens.
 XX
 PN WO9423020-A1.
 XX
 PD 13-OCT-1994.
 XX
 PD 28-MAR-1994; 94WO-JP000495.
 XX
 PF 29-MAR-1993; 93JP-00069988.
 XX
 PF (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Sasaki K, Kurata K, Hanai N, Nishi T;
 XX
 DR WPI; 1994-333182/41.
 XX
 DR N-PSDB; AAQ77831.
 XX
 PT New alpha-2,8-sialyl transferase - useful for producing physiologically
 PT active sugar chains.
 XX
 PS Claim 1; Page 63-66; 102pp; Japanese.
 XX
 CC The amino acid sequence of the novel human alpha-2,8-sialyltransferase.
 CC The gene encodes a protein of 356 a.a. The gene (called WPI) was isolated
 CC from the human melanoma cell line WM266-4 and cloned into the E.coli
 CC plasmid pUC119 to create pUC119.WPI. The gene was inserted into the
 CC expression vector pAMOPRC3Sc to produce the plasmid pAMOPRSWPI. The
 CC missing N-terminal 19 a.a. were inserted into this vector by PCR
 CC amplification using the primers AAQ77835-6. Alpha-2,8-sialyltransferase
 CC is useful in the production of physiologically active sugar chains e.g.
 CC in the conversion of ganglioside GM3 to GD3. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 356 AA;
 Query Match 33.3%; Score 700; DB 2; Length 356;
 Best Local Similarity 43.6%; Pred. No. 1.4e-60;
 Matches 130; Conservative 59; Mismatches 107; Indels 2; Gaps 2;
 QY 99 SEDYLOTITNIQRCPNWRAEYDNPFRKLASCDAIQDFVVSQNTPTVGTNNMSYEVES 158
 DB 53 NEKEIVGVQLQ-QGTAWRRNQTARAFKQMEDCCDPAHLFAMTKMNSPMGKSMWYDGEF 111
 QY 159 KKHIPIRENIFHMPFVSQPFVDYFYNOCVAVGVNGGILNKSICGAEIDKSDFFVRCNLPLPI 218
 DB 112 LYSFTIDNSTVSLFPQATPF-QPLPKKCAVGVNGGILKSCGCRQIDEANFVRCNLPLPL 170
 QY 219 TGSASKDVGSKTNLVTNPSIITKYONLKEKKAQFLEDISTYGDFAFLLPAPFSYRANTG 278
 DB 171 SSEYTKDVGSKQLVTANPSIIRQFQNLWSRKTFTVDNMKIYNHSHIYMPAFSMKTGTE 230
 QY 279 ISFKVYOTLKESKMRQKVLPHRHLALFWRTKGTAYRLSTGLMIASVAVELCENV 338
 DB 231 PSLRVYITLSDVGANQTVLPANFSLRIGKFKWRSRGIHAKRLSTGLFLVSAALGLCEEV 290
 QY 339 KLYGFWPFSTKTIETDPLSHHYDNLMPKGFHOMPKYSQMLQLMRGILKLPFSKCE 396
 DB 291 AIYGFWPFVNMHEQPISSHYYDNLVLPFSGFHAMPPEEFLOLWYLHKIGALRMQLDPCE 348

RESULT 8
 AAB86207
 ID AAB86207 standard; protein; 356 AA.
 XX
 AC AAB86207;

XX 28-AUG-2001 (first entry)
 DT
 XX Human GD3 synthase protein.
 DE
 KW GD3 synthase; human; inhibitor; ganglioside; neurological disorder;
 KW anti-ischemic; cerebral; neurological; anti-neurodegeneration;
 KW antitumor activity; veterinary medicine; cerebral ischemia; stroke;
 KW traumatic brain injury; spinal cord injury; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KW multiple sclerosis; brain tumor
 XX
 OS Homo sapiens.
 XX
 PN DE19958684-A1.
 XX
 PD 07-JUN-2001.
 XX
 PF 06-DEC-1999; 99DE-01058684.
 XX
 PF 06-DEC-1999; 99DE-01058684.
 XX
 PF (KNOL) KNOLL AG.
 XX
 PI Martin-Villalba A, Schenkel J, Kleber S, Testi R;
 XX
 DR WPI; 2001-357289/38.
 XX
 XX Use of ganglioside GD3 synthase inhibitors for treating neurological
 PT diseases, e.g. cerebral ischemia or neurodegeneration.
 PT
 PS Disclosure; Page 10-11; 16pp; German.
 XX
 CC This invention describes a novel use of inhibitors (I) of ganglioside GD3
 CC synthase (II) for treatment of neurological disorders and their
 CC associated indications, symptoms and dysfunctions. The products of the
 CC invention have anti-ischemic, cerebral, neurological,
 CC antineurodegeneration and antitumor activity. (I) are used, in human or
 CC veterinary medicine, to treat cerebral ischemia, (acute) stroke,
 CC traumatic brain or spinal cord injuries, and neurodegenerative diseases
 CC (especially Alzheimer's and Parkinson's diseases, amyotrophic lateral
 CC sclerosis and multiple sclerosis), also brain tumors that cause injury to
 CC the brain. This sequence represents the human GD3 synthase described in
 CC the method of the invention
 XX
 SQ Sequence 356 AA;
 Query Match 33.2%; Score 697; DB 4; Length 356;
 Best Local Similarity 43.3%; Pred. No. 2.9e-60;
 Matches 129; Conservative 60; Mismatches 107; Indels 2; Gaps 2;
 QY 99 SEDYLOTITNIQRCPNWRAEYDNPFRKLASCDAIQDFVVSQNTPTVGTNNMSYEVES 158
 DB 53 NEKEIVGVQLQ-QGTAWRRNQTARAFKQMEDCCDPAHLFAMTKMNSPMGKSMWYDGEF 111
 QY 159 KKHIPIRENIFHMPFVSQPFVDYFYNOCVAVGVNGGILNKSICGAEIDKSDFFVRCNLPLPI 218
 DB 112 LYSFTIDNSTVSLFPQATPF-QPLPKKCAVGVNGGILKSCGCRQIDEANFVRCNLPLPL 170
 QY 219 TGSASKDVGSKTNLVTNPSIITKYONLKEKKAQFLEDISTYGDFAFLLPAPFSYRANTG 278
 DB 171 SSEYTKDVGSKQLVTANPSIIRQFQNLWSRKTFTVDNMKIYNHSHIYMPAFSMKTGTE 230
 QY 279 ISFKVYOTLKESKMRQKVLPHRHLALFWRTKGTAYRLSTGLMIASVAVELCENV 338
 DB 231 PSLRVYITLSDVGANQTVLPANFSLRIGKFKWRSRGIHAKRLSTGLFLVSAALGLCEEV 290
 QY 339 KLYGFWPFSTKTIETDPLSHHYDNLMPKGFHOMPKYSQMLQLMRGILKLPFSKCE 396
 DB 291 AIYGFWPFVNMHEQPISSHYYDNLVLPFSGFHAMPPEEFLOLWYLHKIGALRMQLDPCE 348

RESULT 9

ADD48076
ID ADD48076 standard; protein; 380 AA.
XX AC
XX ADD48076;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
XX Human Protein XP_008782, SEQ ID NO 13773.
XX
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS Unidentified.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GHEO) GEN HOSPITAL CORP.
PA (PABB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
DR GENBANK; XP_008782.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Example 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 380 AA;
XX
XX Query Match 22.7%; Score 477.5; DB 7; Length 380;
XX Best Local Similarity 34.5%; Pred. No. 2.6e-38;
XX Matches 114; Conservative 55; Mismatches 130; Indels 31; Gaps 10;

QY 85 QYSLNSLNKTRYSEDDYLOTTIN-----IQRCP--WNRQAEYDNFRAKLASCCDAIQ 137
DB 62 QFALKFL-----DPGFVP--NSLTQELQKPKSKWTFNRFTAFLHOROEILOHVDVIK 112
QY 138 DFVVSQNTTPVGTNMSYEVESEKHI-PIRENIHFHMFVSOPFDVDPYNQCAVVGNGGILN 196
DB 113 NFSLTNSVRIGOLMHDYSSHAFVFSISNNFSLPDPVSPIMNKHYNICAVVGNSGILT 172
QY 197 KSLCGAIDKSDVFRCNLPPIITSSASKDVGSKTNLVTNPSIITLKYNLK--EKKAQF 254
DB 173 GSQCGQEQIDKSDVFRCNFAP--TEAFQDVGRKTNLTTFNPISILEKYNNLLTIQDRNFF 231
QY 255 LEDISTYGDFAFLLPAPFSYRANVTESFKYVQTLKESKMRQKVLFFHP-RVLRHLALFWRT 313
DB 232 FLSLKXLDGAILWIPAFFHTSPVTRTLVDFVFRHGRQKLVQLAWPGNIMQHVNRWKN 291
QY 314 KGVTAVRLSTGLMIASVAVELCEVLYGFWPFS---KTIEDTPLSHHYDNNMLPK--- 366
DB 292 KHLSPRLSTGILMYTLASNAICSEIHLYGFWPFGFDNTREDLP--YHYDCKGKTETTK 349
QY 367 -HGFHQPKEYSQMLQLMRGILKLOFSKC 395
DB 350 WQESHQLPRAEFQLLYRMHGEGLTJLTLSHC 379
RESULT 10
ADD48074
ID ADD48074 standard; protein; 380 AA.
XX AC ADD48074;
XX
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
XX Rat Protein AAB50061, SEQ ID NO 13771.
DE
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
OS Unidentified.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GHEO) GEN HOSPITAL CORP.
PA (PABB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
DR GENBANK; AAB50061.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Example 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 380 AA;

XX PD 22-NOV-2001.
 XX 18-MAY-2001; 2001WO-JP004192.
 XX 18-MAY-2000; 2000JP-00145977.
 XX (UTNI-) UNIV NIHOON SCHOOL JURIDICAL PERSON.
 XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX WPI; 2002-034733/04.
 XX N-PSDB; ABI99514.
 XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 XX Claim 2; Page 1379-1381; 2690pp; English.
 XX The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
 CC protein sequences in AB57020 to AB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX Sequence 380 AA;

Query Match 22.4%; Score 470; DB 5; Length 380;
 Best Local Similarity 33.1%; Pred. No. 1.4e-37;
 Matches 113; Conservative 58; Mismatches 128; Indels 42; Gaps 10;
 QY 69 YLDEKTTQITEKCKDQVSVQNTTGVGNTMSYEVESKKHI-PIRENIHMFVPVSOPFVDYPNQ 126
 DB 67 FLDOQSFVPIIT-----NSLTHTHE-----LQKPSKWTNRTAFHLQR 101
 QY 127 AKLASCDDAIQDFVSVQNTTGVGNTMSYEVESKKHI-PIRENIHMFVPVSOPFVDYPNQ 185
 DB 102 QEILQHVVDVINKFSLTKSSVRIQGLMHYDYSKHYVFSISNNFSLLPDVSPIKKRYNV 161
 QY 186 CAVVNGGILNKLSCGAEIDKSDVFRNLPPIITGSASKOVGSKTNLVTNPSIITLKYQ 245
 DB 162 CAVVNGSGILTSQCGQEIIDKSDVFRNLPPIITGSASKOVGSKTNLVTNPSIITLKYQ 220
 QY 246 NLK--EKAQPLEDISYGDFAILLPAPSYANTGISEKVVQTLKESQWOKVLPFP-R 302
 DB 221 NLLTIQDRNNFSLKXLDGAILIPAFFFTSATVTRTLVDFVFRGQLKVLQWAPGN 280
 QY 303 YLRHLAFWRFTKGTAVRLSLGLMIASVAVLCECNKLYIGFWPFS---KTEDTPLSHHY 359
 DB 281 IMQHVNRVWKVKKHLSPKRLSGILMYLTAISCEIHLHYGFWPFPDNTREDLP--YHY 338
 QY 360 YDNNMLPK-----HGFHQMPEKYSQMLQLHMRGILKLQFSKC 395
 DB 339 YDKGKTFTTKWQSHQLPAEFQQLLYRMHGSGLTKLTLSHC 379
 RESULT 13
 AAW05300
 ID AAW05300 standard; protein; 381 AA.
 XX
 AC AAW05300;
 XX

DT 17-FEB-1997 (revised)
 DT 17-DEC-1996 (first entry)
 DE Sia alpha 2,3Gal Beta 1,4GlcNAc alpha 2,8-sialyltransferase.
 KW Sialyltransferase; oligosialic acids; protein; glycoprotein; glycolipid;
 KW sugar; biosynthesis; cancer; metastasis; spermatozoa; inflammation;
 KW nervous tissue.
 XX Mus musculus.
 XX Key Location/Qualifiers
 FH Peptide 1..16
 FT /note= "Signal peptide"
 FT Protein 17..381
 FT /note= "Mature Protein, claim 1"
 FT Domain 18..33
 FT /note= "Putative transmembrane domain"
 FT Modified-site 93
 FT /note= "Potential N-glycosylation site"
 FT Modified-site 113
 FT /note= "Potential N-glycosylation site"
 FT Region 161..205
 FT /label= Sialyl motif L
 FT Modified-site 206
 FT /label= Potential N-glycosylation site
 FT Region 301..323
 FT /label= Sialyl motif S
 PN EP736602-A2.
 XX 09-OCT-1996.
 PD 02-APR-1996; 96EP-00105267.
 PF 03-APR-1995; 95JP-00077469.
 PR (RIKA) INST PHYSICAL & CHEM RES
 PA Tsuji S, Yoshida Y, Kojima N, Kurosawa N, Hamamoto T;
 PI WPI; 1996-444889/45.
 XX N-PSDB; AAT39663.
 DR New isolated sialyltransferase enzyme - useful for treating e.g.
 DR hereditary diseases, cancer metastasis, inflammatory reactions or nervous
 PT tissues.
 PT Claim 1; Fig 1; 25pp; English.
 PS The sialyltransferase (SST) is useful as an agent for introducing
 XX oligosialic acids such as di-, tri- or tetra-sialic acids into proteins,
 CC glycoproteins or glycolipids. It can be used in the treatment of
 CC hereditary diseases which involve the lack of enzymes needed for the
 CC biosynthesis of specified sugar chains. It can also be used for the
 CC prevention of cancerous metastasis, maturation of sperm, inhibition of
 CC inflammatory reactions or regeneration and reactivation of nervous
 CC tissues. Revised 19-FEB-1997 for inclusion of full length protein
 CC sequence and features table information
 XX Sequence 381 AA;
 SQ

Query Match 22.4%; Score 470; DB 2; Length 381;
 Best Local Similarity 33.1%; Pred. No. 1.4e-37;
 Matches 113; Conservative 58; Mismatches 128; Indels 42; Gaps 10;
 QY 69 YLDEKTTQITEKCKDQVSVQNTTGVGNTMSYEVESKKHI-PIRENIHMFVPVSOPFVDYPNQ 126
 DB 68 FLDOQSFVPIIT-----NSLTHTHE-----LQKPSKWTNRTAFHLQR 102
 QY 127 AKLASCDDAIQDFVSVQNTTGVGNTMSYEVESKKHI-PIRENIHMFVPVSOPFVDYPNQ 185
 DB 103 QEILQHVVDVINKFSLTKSSVRIQGLMHYDYSKHYVFSISNNFSLLPDVSPIKKRYNV 162

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 359 AA;

Query Match 19.9%; Score 418.5; DB 7; Length 359;
Best Local Similarity 28.9%; Pred. No. 1.8e-32;
Matches 107; Conservative 77; Mismatches 161; Indels 25; Gaps 9;
QY 37 MEGSREDTSGTAAKTLWSPPTVPTRTRNSTYLDEKTTQIT---EKCKDQYSLNLSLN 93
DB 1 MRSIRKRWITCTISLLIFPKTEIARTE-----EHQETQLIGDGLC--LSRSLVNSSD 53
QY 94 KTRYSEDDYLOQTITNQCPCWNRQAEYDNFRAKLASCCDAIQDFVVSQNNTPVGTNMS 153
DB 54 KIIRKAGSTIFQ--HSVQ--GWKINSLSLVLIRKNILRFLDAERDVSVKSPKPGDVH 109
QY 154 YEVEKXHIPIRENI FHMFPVQPFVDYPYNOCAVGVNGGILNKLSCGAIDKSDVFRC 213
DB 110 YVLDRRRTLNISHLNLSLPEVSPMKRRFKTCVAVGNSGILLDSGCGKEIDSHNFVIRC 169
QY 214 NLPPTIGSASKDVGSKTNLVNPSIITLKYNLKEK--KAQFLEDISTYGDAPFLLPAP 271
DB 170 NLAPVVEFAA-DVGTKSDFTIMNPSVVQRAFGGFRNESDREKFVHRLSMLNDSVLWIPAF 228
QY 272 SYRANTGISFKVYQTLKESKMRQKVLFFHPHYLRHLALFWRTKGVTAIRLSTGLMTASVA 331
DB 229 MVRGGEKHVEWVNALILKNKLQVRTAYPSLRLIHAVRGYWLTKVPIKRPSTGLLMYTLA 288
QY 332 VELCENVKLIGFWPFPFTIEDTPLSHHYNDMLPKHGF-----HQPKEYSQMLQLHMR 385
DB 289 TRFCDEIHLYGFWPFPKPKDLNGAKVKHYHDDL--KYRYFSNASPHRMPLEFKTLNVLHNR 346
QY 386 GILKLQFSKC 395
DB 347 GALKLTGKC 356

Search completed: May 26, 2006, 23:25:39
Job time : 201 secs

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OM protein - protein search, using sw model

Run on: May 26, 2006, 23:31:05 ; Search time 50 Seconds
(without alignments)
696.744 Million cell updates/sec

Title: US-10-501-930-1
Perfect score: 2102
Sequence: 1 MRSGGTLFALIGSLMLLLLL.....MLQLHWRGILKQFSKQETA 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /EMC_Celerra_SID33/ptodata/2/iaa/5 COMB.pep.*
2: /EMC_Celerra_SID33/ptodata/2/iaa/6 COMB.pep.*
3: /EMC_Celerra_SID33/ptodata/2/iaa/7 COMB.pep.*
4: /EMC_Celerra_SID33/ptodata/2/iaa/H COMB.pep.*
5: /EMC_Celerra_SID33/ptodata/2/iaa/PCTUS COMB.pep.*
6: /EMC_Celerra_SID33/ptodata/2/iaa/RE COMB.pep.*
7: /EMC_Celerra_SID33/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	705	33.5	368	2	US-09-949-016-8001 Sequence 8001, Ap
2	700	33.3	356	2	US-09-949-016-6307 Sequence 6307, Ap
3	697	33.2	356	2	US-08-361-304A-2 Sequence 2, Appli
4	470	22.4	339	1	US-08-626-994A-3 Sequence 3, Appli
5	470	22.4	339	2	US-08-957-742-3 Sequence 3, Appli
6	470	22.4	364	1	US-08-626-994A-1 Sequence 1, Appli
7	470	22.4	364	2	US-08-957-742-1 Sequence 1, Appli
8	419.5	20.0	359	1	US-08-503-133A-2 Sequence 2, Appli
9	419.5	20.0	359	1	US-08-972-775A-2 Sequence 2, Appli
10	419.5	20.0	359	1	US-08-972-775A-2 Sequence 2, Appli
11	419.5	20.0	359	2	US-08-989-545-2 Sequence 2, Appli
12	419.5	20.0	429	2	US-09-949-016-10541 Sequence 10541, A
13	408.5	19.4	384	2	US-09-949-016-9465 Sequence 9465, Ap
14	389	18.5	375	1	US-08-446-875-8 Sequence 8, Appli
15	389	18.5	375	1	US-08-102-385G-8 Sequence 8, Appli
16	352.5	16.8	222	1	US-08-446-875-14 Sequence 14, Appli
17	221	10.5	600	2	US-09-991-181-347 Sequence 347, App
18	221	10.5	600	2	US-09-990-444-347 Sequence 347, App
19	221	10.5	600	2	US-09-997-333-347 Sequence 347, App
20	221	10.5	600	2	US-09-992-598-347 Sequence 347, App
21	221	10.5	600	2	US-09-989-735-347 Sequence 347, App
22	221	10.5	600	3	US-09-989-726-347 Sequence 347, App
23	221	10.5	600	3	US-09-997-514-347 Sequence 347, App
24	221	10.5	600	3	US-09-989-728-347 Sequence 347, App
25	221	10.5	600	3	US-09-997-349-347 Sequence 347, App
26	221	10.5	600	3	US-09-997-653-347 Sequence 347, App

ALIGNMENTS

RESULT 1

US-09-949-016-8001
; Sequence 8001, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,765
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,428
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8001
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8001

Query Match 33.5%; Score 705; DB 2; Length 368;
Best Local Similarity 39.4%; Pred. No. 3.5e-67;
Matches 146; Conservative 64; Mismatches 145; Indels 16; Gaps 6;

QY	26	PADAPARSRLMGSRDTSSTALKTLSPTTPVTRNSTYLDKTTOTTEKCDLQ	85
DB	6	PWDAGAMSPCGARRRRTSGAMAVL--AWK----FPRTR--LPMGASALCVVLCWLYI	57
QY	86	YSLNSLSNKTTRYSEDDYLQTIQICPWNQAEYDNFRKASCCDAIQDFVVSQNN	145
DB	58	FPVYRLPN-----EKEIVQGVLD--QGTAMRNQTAARAFKQMEDCCDPAHLFAMTYKN	110
QY	146	TPVGTNMSYEVESKHHIPRENIHMPVSPQFVDYPPNCAVVGNGGILNKSICGABID	205
DB	111	SPMGKSNWYDGEFLYSFTIDNSTSLFQATPF--QLPLKTCVAVVGNGGILKSCGGRQID	169
QY	206	KSDVFRCNLPPTTGSASDVGSNTLVNTPSTITLKYONLKEKAQFLEDISTYDGF	265
DB	170	EAMFVRCNLPPTTGSASDVGSNTLVNTPSTITLKYONLKEKAQFLEDISTYDGF	229
QY	266	LLLPAPSYRANTGTSFKVYOTLAKSKMRQKVLFPHPYRLHLLFWRTKGVTAIRLSTGL	325
DB	230	IYMPAFSMKTGTSPSLRVYVTLSSVGNQTVLPANPNFLRSIGKFWKSRGHHAKRLSTGL	289

Qy 326 MIASVAVELCNVLYGFWPFSKTIETDPLSHHYDNNLPHKGHPQKPEYQMLQLHMR 385
Db 290 FLVSAALGLCEVAIYGFWPFSVNMHEQPISHHYDNNLVPFSGFHAMPBFLQLWYLHKI 349
Qy 386 GILKLOFSKCE 396
Db 350 GALKRQLDPCE 360

RESULT 2

US-09-949-016-6307
; Sequence 6307, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6307
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6307

Query Match 33.3%; Score 700; DB 2; Length 356;
Best Local Similarity 43.6%; Pred. No. 1.2e-66;
Matches 130; Conservative 59; Mismatches 107; Indels 2; Gaps 2;

Qy 99 SEDYLQTTIQRCPNRAEQEYDNRFRKLASCCDAIQDFVVSQNNTPVGTNMSYEVS 158
Db 53 NEKEIVQGVQLQ-QGTARRNQTPAARFKQMEDCCDPAHLFAMTKMNSPMGKSMWYDGEF 111
Qy 159 KKHIPRENIHFHPPVQDFVYPYNOCAVVGNGGILNKLSCGAEIDKSDVFRCLNLPPI 218
Db 112 LYSFTIDNSTYSLFPQATPF-QPLKKAQVVGNGGILKSGCGRQIDEANFVMRCNLPPL 170
Qy 219 TGSASDVGSKTNLVTNPSIITLKYONLKEKKAQFLEDISTYGDAPFLLLPAPFSYRANTG 278
Db 171 SBYTKDVGSKQLVTANPSIIRQRFQNLWSRKTVDNNKIYNHSIYNPFSMTGTGE 230
Qy 279 ISPKVYOTLKESKMRQKVLFFHPRYLRHLALFWRKTGVTAYRLSTGLMIASVAVELCENV 338
Db 231 PSRLVYVYTLSDVGANQVLFANFNFLASIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEV 290
Qy 339 KLYGFWPFSKTIETDPLSHHYDNNLPHKGHPQKPEYQMLQLHMRGILKLOFSKCE 396
Db 291 AIYGFWFPFSVNMHEQPISHHYDNNLVPFSGFHAMPBFLQLWYLHKI GALKRQLDPCE 348

RESULT 3

US-08-361-304A-2
; Sequence 2, Application US/08361304A
; Patent No. 6596523
; GENERAL INFORMATION:
; APPLICANT: SASAKI, KATSUTOSHI
; APPLICANT: MIURA, KAZUMI
; APPLICANT: HANAI, NOBUO
; APPLICANT: NISHI, TATSUNARI
; TITLE OF INVENTION: -2,8-STALYLTRANSFERASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #110, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361304A
FILING DATE: 29-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00495
FILING DATE: 28-MAR-1994
APPLICATION NUMBER: JP HEI-5-9988
FILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-86
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 356
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-361-304A-2

Query Match 33.2%; Score 697; DB 2; Length 356;
Best Local Similarity 43.3%; Pred. No. 2.5e-66;
Matches 129; Conservative 60; Mismatches 107; Indels 2; Gaps 2;

Qy 99 SEDYLQTTIQRCPNRAEQEYDNRFRKLASCCDAIQDFVVSQNNTPVGTNMSYEVS 158
Db 53 NEKEIVQGVQLQ-QGTARRNQTPAARFKQMEDCCDPAHLFAMTKMNSPMGKSMWYDGEF 111
Qy 159 KKHIPRENIHFHPPVQDFVYPYNOCAVVGNGGILNKLSCGAEIDKSDVFRCLNLPPI 218
Db 112 LYSFTIDNSTYSLFPQATPF-QPLKKAQVVGNGGILKSGCGRQIDEANFVMRCNLPPL 170
Qy 219 TGSASDVGSKTNLVTNPSIITLKYONLKEKKAQFLEDISTYGDAPFLLLPAPFSYRANTG 278
Db 171 SBYTKDVGSKQLVTANPSIIRQRFQNLWSRKTVDNNKIYNHSIYNPFSMTGTGE 230
Qy 279 ISPKVYOTLKESKMRQKVLFFHPRYLRHLALFWRKTGVTAYRLSTGLMIASVAVELCENV 338
Db 231 PSRLVYVYTLSDVGANQVLFANFNFLASIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEV 290
Qy 339 KLYGFWPFSKTIETDPLSHHYDNNLPHKGHPQKPEYQMLQLHMRGILKLOFSKCE 396
Db 291 AIYGFWFPFSVNMHEQPISHHYDNNLVPFSGFHAMPBFLQLWYLHKI GALKRQLDPCE 348

RESULT 4

US-08-626-994A-3
; Sequence 3, Application US/08626994A
; Patent No. 5798244
; GENERAL INFORMATION:
; APPLICANT: TSUJI et al.
; TITLE OF INVENTION: Sia' 2,3Gal' 1,4GlcNAc ' 2,8-
; TITLE OF INVENTION: SIALYLTRANSFERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenblum & Bernstein, P.L.C.
; STREET: 1941 Roland Clarke Place
; CITY: Reston
; STATE: Virginia

COUNTRY: U.S.A.
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,994A
FILING DATE: April 3, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
TELEFAX: (703) 716-1180
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-08-626-994A-3

Query Match 22.4%; Score 470; DB 1; Length 339;
Best Local Similarity 33.1%; Pred. No. 7.8e-42;
Matches 113; Conservative 58; Mismatches 126; Indels 42; Gaps 10;
QY 69 YLDEKTTQTECKCKDQYSLNSLNKTRRYSEDDYLOITITNIQRCP--WNRQAEYDNP 126
DB 26 FLDQSFVPI-----NSLTHE-----LQEKPSKWTNRTAFHQ 60
QY 127 AKLASCCDAIQDFVVSQNTPTVGTNMSYEVSCKGHI-PIRENIHFMPVQFVDPY 185
DB 61 QEILQHDVIVKFNLSKSSVRIGOLMHYDYSSHKYVFSINNFRSLLPDVPSPIMNKRYN 120
QY 186 CAVVNGGILNKLSCGAIDKSDVFCNLPITGSASKDVGSKTNLVTNPSIITLKYQ 245
DB 121 CAVVNSGILTGSCGQGEIDKSDVFCNLPITGSASKDVGSKTNLVTNPSIITLKYQ 179
QY 246 NLK--EKAQFLEDISTYGDAPFLPAPFSYRANTGISFKVYQTLKESKMRQKVLFFHP-R 302
DB 180 NLLTIQDRNNEFLSKKLDGAILWIPAFFHTSATVTRTLVDFFVHGRGOLKVLAWPGN 239
QY 303 YLRHLALFWRKGTAVYRLSTGLMTASVAVLCEENVKLYGFWPPFS---KTIEDTPLSHY 359
DB 240 IMQHVNRVYKKNKLSPKRLSTGLMYTLASAICEIHLGYFWPPFGFDPNTREDLP--YHY 297
QY 360 YDNMLPK-----HGPHQMPKEYSOMLQHMRLGILKQFSKC 395
DB 298 YDKKGTFTTKWQESHQLPFAEQLLYRMHGBGLTKLTLSHC 338

RESULT 5
US-08-957-742-3
Sequence 3, Application US/08957742
Patent No. 6017743
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4G1CNAC ' 2,8-
TITLE OF INVENTION: SIALYLTRANSFERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
CITY: Reston
STATE: Virginia
COUNTRY: U.S.A.

ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,742
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
TELEFAX: (703) 716-1180
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-08-957-742-3

Query Match 22.4%; Score 470; DB 2; Length 339;
Best Local Similarity 33.1%; Pred. No. 7.8e-42;
Matches 113; Conservative 58; Mismatches 126; Indels 42; Gaps 10;
QY 69 YLDEKTTQTECKCKDQYSLNSLNKTRRYSEDDYLOITITNIQRCP--WNRQAEYDNP 126
DB 26 FLDQSFVPI-----NSLTHE-----LQEKPSKWTNRTAFHQ 60
QY 127 AKLASCCDAIQDFVVSQNTPTVGTNMSYEVSCKGHI-PIRENIHFMPVQFVDPY 185
DB 61 QEILQHDVIVKFNLSKSSVRIGOLMHYDYSSHKYVFSINNFRSLLPDVPSPIMNKRYN 120
QY 186 CAVVNGGILNKLSCGAIDKSDVFCNLPITGSASKDVGSKTNLVTNPSIITLKYQ 245
DB 121 CAVVNSGILTGSCGQGEIDKSDVFCNLPITGSASKDVGSKTNLVTNPSIITLKYQ 179
QY 246 NLK--EKAQFLEDISTYGDAPFLPAPFSYRANTGISFKVYQTLKESKMRQKVLFFHP-R 302
DB 180 NLLTIQDRNNEFLSKKLDGAILWIPAFFHTSATVTRTLVDFFVHGRGOLKVLAWPGN 239
QY 303 YLRHLALFWRKGTAVYRLSTGLMTASVAVLCEENVKLYGFWPPFS---KTIEDTPLSHY 359
DB 240 IMQHVNRVYKKNKLSPKRLSTGLMYTLASAICEIHLGYFWPPFGFDPNTREDLP--YHY 297
QY 360 YDNMLPK-----HGPHQMPKEYSOMLQHMRLGILKQFSKC 395
DB 298 YDKKGTFTTKWQESHQLPFAEQLLYRMHGBGLTKLTLSHC 338

RESULT 6
US-08-626-994A-1
Sequence 1, Application US/08626994A
Patent No. 5798244
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4G1CNAC ' 2,8-
TITLE OF INVENTION: SIALYLTRANSFERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
CITY: Reston
STATE: Virginia

ZIP: 20191
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 1.44 diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word Perfect 5.1+ (ASCII)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/957,742
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/626,994
 FILING DATE: April 3, 1996
 APPLICATION NUMBER: JP 77469/1995
 FILING DATE: April 3, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Arnold Turk
 REGISTRATION NUMBER: 33,094
 REFERENCE/DOCKET NUMBER: P14565
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 716-1191
 TELEFAX: (703) 716-1180
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 364 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 US-08-957-742-1

	Query Match	22.4%	Score 470;	DB 2;	Length 364;
	Best Local Similarity	33.1%	Prog. No. 8.7e-42;		
	Matches 113;	Conservative 59;	Mismatches 128;	Indels 42;	Gaps 10
Qy	69	YLDEKTYOITEKCKDLOYSLNSINENKTRRYSRDDYLOTTINICRCP--WNRQAEYDNFR	126		
		:	:	:	:
Db	51	FLDQSFVPII-----NSIPIH-----	85		
		:	:	:	:
		:	:	:	:
		:	:	:	:
Qy	127	AKLASCCDAIQDFVSVONTPVGNNSYEVESKKHI-PIRENIPHPVPVSOFPVDYPYNQ	185		
		:	:	:	:
		:	:	:	:
Db	86	QEILQHVVDVINKFSLTKSSVRICQLMHYDYSKHVFSINNFRLSLDPDVSPIWKRNV	145		
		:	:	:	:
		:	:	:	:
Qy	186	CAVVGNGIILINKLSCGAIEDKSLFVFRCNLPPIITGASAKDVGSKTNLTVNPSITLKYQ	245		
		:	:	:	:
		:	:	:	:
Db	146	CAVVGNSGIUTGQCQGEIDKSLFVSRCNFAP-TEAFHKDVGKTNLTTFNPSILEKYYN	204		
		:	:	:	:
		:	:	:	:
Qy	246	NLK--EKKAQFIEDISTYGDFAFLPAPFSYRANTGISFKVYQTLKESKMRQKVLFFHP-R	302		
		:	:	:	:
		:	:	:	:
Db	205	NLTIQDRNNFFLSLKKLDGAILNIPAFFHTSATVTRLVDVFEHGRQLKVQLAWPGN	264		
		:	:	:	:
		:	:	:	:
Qy	303	YLRLHALFWRTKGVTAAYRLSTGTMASAVAVELCENVKLYGFWPSPS-----KTIEDTPLSHHY	359		
		:	:	:	:
		:	:	:	:
Db	265	IMQHVNRVYKMKHLSPKRLSTGLMYTLASACIEEIHLYGFWPFGFDPNTRDPLP--YHY	322		
		:	:	:	:
		:	:	:	:
Qy	360	YDNMLPK-----HGFQMPKKEYSMLQLHMRGILKLQFSKC	395		
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	323	YDKKGTKFTTKQWESHOLPAEFCULLYMRMHGEGTLKLTLSHC	363		
		:	:	:	:
		:	:	:	:

RESULT 8
 US-08-503-133A-2
 ; Sequence 2, Application US/08503133A
 ; Patent No. 5747326
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;
 ; APPLICANT: Nakayama, Jun; Eckhardt, Matthias
 ; TITLE OF INVENTION: Isolated Polysialyl Transferases,
 ; TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
 ; TITLE OF INVENTION: Production and Use
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue

; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/503.133A
; FILING DATE: 17-JULY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/503.133
; FILING DATE: 17-JULY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/04289
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5747336man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-503-133A-2

Query Match 20.0%; Score 419.5; DB 1; Length 359;
Best Local Similarity 28.9%; Pred. No. 2.4e-36;
Matches 107; Conservative 78; Mismatches 160; Indels 25; Gaps 9;

QY 37 MEGSREDTSGTSAALKTLWSPTTPVPRTRNSTYLDKTKTQIT---EKCKDLOYSLNSLN 93
DB 1 MRSIRKRWITICTISLLIFKYKTEIARTE-----EHQETQLIGDGLC--LSRSLVNSSD 53
QY 94 KTRYSEDDYLTQITNIQRCFWRQAEYDNFRAKLASCCDAIOFVVVSQNNTPVGTNMS 153
DB 54 KIIRKAGSTIFQ--HSVQ--GWRINSSLVLEIRKNILRFLDAERDVSVVKSSEKFGDVIH 109
QY 154 YEVESSKHPIRENIHFMPVSPQPDYYPNQCAVVGNGIILKSLCAEIDKSDVFVPRC 213
DB 110 YVLDERRRLTNIHDLHSLPEVSPMKNRRFKTCAVVGNSGILLDSGCCGKEIDSHNFVIRC 169
QY 214 NLPITGSASKDVGSKTNLVNPSIIITLKYQNLKEK--KAQFLEDISTYGDALLPAP 271
DB 170 NLAPEVVEFAA--DVGTGSDFITMNPVSQVQAFGGFNRSDRAKFVHRLSMLNDSVLWIAP 228
QY 272 SYRANTGISPKVYQTLKESKMRQKLVLPFPHRYLRHLALFWRTKGVTAVALSTGLMIASVA 331
DB 229 MVKGEKHEVWVNNALIKNKLKVRTAYPSLRLIHAVRGYWLTKNPKPIKEPSTGLMYTLA 288
QY 332 VELCENVKLYGFWPFSKTIETDPLSHHYDNMLPKHGF-----HOMPKEYSQMLQLHNR 385
DB 289 TRFCDEIHLGYFWPPPKDLNGKAVKYHYDDL--KYRYFSNASPHRMPLEFKTLNVLNHR 346
QY 386 GILKLOQSKC 395
DB 347 GALKLTTGKC 356

RESULT 9

US-08-576-775A-2
; Sequence 2, Application US/08576775A
; Patent No. 5849904
; GENERAL INFORMATION:

; APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;
; APPLICANT: Nakayama, Jun; Eckhardt, Matthias
; TITLE OF INVENTION: Isolated Polysialyl Transferases,
; TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of

; TITLE OF INVENTION: Production and Use
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/576.775A
; FILING DATE: 21-December-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/503.133
; FILING DATE: 17-JULY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/04289
; FILING DATE: 22-December-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5849904man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1050.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-576-775A-2

Query Match 20.0%; Score 419.5; DB 1; Length 359;
Best Local Similarity 28.9%; Pred. No. 2.4e-36;
Matches 107; Conservative 78; Mismatches 160; Indels 25; Gaps 9;

QY 37 MEGSREDTSGTSAALKTLWSPTTPVPRTRNSTYLDKTKTQIT---EKCKDLOYSLNSLN 93
DB 1 MRSIRKRWITICTISLLIFKYKTEIARTE-----EHQETQLIGDGLC--LSRSLVNSSD 53
QY 94 KTRYSEDDYLTQITNIQRCFWRQAEYDNFRAKLASCCDAIOFVVVSQNNTPVGTNMS 153
DB 54 KIIRKAGSTIFQ--HSVQ--GWRINSSLVLEIRKNILRFLDAERDVSVVKSSEKFGDVIH 109
QY 154 YEVESSKHPIRENIHFMPVSPQPDYYPNQCAVVGNGIILKSLCAEIDKSDVFVPRC 213
DB 110 YVLDERRRLTNIHDLHSLPEVSPMKNRRFKTCAVVGNSGILLDSGCCGKEIDSHNFVIRC 169
QY 214 NLPITGSASKDVGSKTNLVNPSIIITLKYQNLKEK--KAQFLEDISTYGDALLPAP 271
DB 170 NLAPEVVEFAA--DVGTGSDFITMNPVSQVQAFGGFNRSDRAKFVHRLSMLNDSVLWIAP 228
QY 272 SYRANTGISPKVYQTLKESKMRQKLVLPFPHRYLRHLALFWRTKGVTAVALSTGLMIASVA 331
DB 229 MVKGEKHEVWVNNALIKNKLKVRTAYPSLRLIHAVRGYWLTKNPKPIKEPSTGLMYTLA 288
QY 332 VELCENVKLYGFWPFSKTIETDPLSHHYDNMLPKHGF-----HOMPKEYSQMLQLHNR 385
DB 289 TRFCDEIHLGYFWPPPKDLNGKAVKYHYDDL--KYRYFSNASPHRMPLEFKTLNVLNHR 346
QY 386 GILKLOQSKC 395
DB 347 GALKLTTGKC 356

RESULT 10

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US-08-972-498-2
; Sequence 2, Application US/08972498
; Patent No. 5959078
; GENERAL INFORMATION:
; APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;
; APPLICANT: Nakayama, Jun; Eckhardt, Matthias
; TITLE OF INVENTION: Isolated Polysialyl Transferases,
; TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
; TITLE OF INVENTION: Production and Use
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,498
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/576,775
; FILING DATE: 21-December-1995
; APPLICATION NUMBER: 08/503,133
; FILING DATE: 17-July-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/04289
; FILING DATE: 22-December-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5959078man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1050.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-972-498-2

Query Match 20.0%; Score 419.5; DB 1; Length 359;
Best Local Similarity 28.9%; Pred. No. 2.4e-36;
Matches 107; Conservative 78; Mismatches 160; Indels 25; Gaps 9;

Qy 37 MEGSRETSGTSAAKLTWSPPTVPTRNSTYLDKTTQIT---EKCKDQYSLNSLN 93
Db 1 MRSIRKRWITCTISLLIFYKTKIARTE-----EHOETQIGDGLC--LSRLVNSSD 53
Qy 94 KTRYSEDDYLOITNIQRCPPWRQAEYDNFRKLASCCDAIQDFVVSQNNTPVGTNMS 153
Db 54 KIIRKAGSTIFQ--HSVQ--GWRINSSVLVIRKNILRFLDAERDVSVVKSSFPGDVIH 109
Qy 154 YEVESSKXHIPRENIHFHMFVPSQFVDYVPYNOCAVVGNGGILNKLSCGAEDKSDVFVRC 213
Db 110 YVLDRRRTLNISHLHSLLEPVSMPKRRRFTCAVVGNSGILLDSGGCKEIDSHNFVIRC 169
Qy 214 NLPPTGSASCKVSGKTNLVTVA--KAQFLEDISTYGDALLPAP 271
Db 170 NLAPVVEFAA--DVGTGKSDFITMPSVVQRAFGGFRNESDRAKFVHRLSMLNDSVLWIPAF 228
Qy 272 SYRANTGISFVYQTLKESKMRQKVLFPHPYRLHALFWRTKGTAYRLSTGLMIASVA 331
Db 229 MVKGGKHVEVWNLILKNKLKVRTAYPSLRLIHAVRGYWLTKVPIKRPSTGLLMYTLA 288

US-08-972-498-2
; Sequence 2, Application US/08899545
; Patent No. 6020201
; GENERAL INFORMATION:
; APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;
; APPLICANT: Nakayama, Jun; Eckhardt, Matthias
; TITLE OF INVENTION: Isolated Polysialyl Transferases,
; TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
; TITLE OF INVENTION: Production and Use
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,545
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/503,133
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6020201man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-545-2

Query Match 20.0%; Score 419.5; DB 2; Length 359;
Best Local Similarity 28.9%; Pred. No. 2.4e-36;
Matches 107; Conservative 78; Mismatches 160; Indels 25; Gaps 9;

Qy 37 MEGSRETSGTSAAKLTWSPPTVPTRNSTYLDKTTQIT---EKCKDQYSLNSLN 93
Db 1 MRSIRKRWITCTISLLIFYKTKIARTE-----EHOETQIGDGLC--LSRLVNSSD 53
Qy 94 KTRYSEDDYLOITNIQRCPPWRQAEYDNFRKLASCCDAIQDFVVSQNNTPVGTNMS 153
Db 54 KIIRKAGSTIFQ--HSVQ--GWRINSSVLVIRKNILRFLDAERDVSVVKSSFPGDVIH 109
Qy 154 YEVESSKXHIPRENIHFHMFVPSQFVDYVPYNOCAVVGNGGILNKLSCGAEDKSDVFVRC 213
Db 110 YVLDRRRTLNISHLHSLLEPVSMPKRRRFTCAVVGNSGILLDSGGCKEIDSHNFVIRC 169
Qy 214 NLPPTGSASCKVSGKTNLVTVA--KAQFLEDISTYGDALLPAP 271
Db 170 NLAPVVEFAA--DVGTGKSDFITMPSVVQRAFGGFRNESDRAKFVHRLSMLNDSVLWIPAF 228
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QY 272 SYRANTGISFKYQTLKSKKQKQKLVLFPHPRYLRLHALFWRTKGTAYRLSTGLMIASVA 331
DB 229 MYGGEKHEVWVNAIILKNKLVKRTAYPSLRSLIHAHVRGYWLTNKNVPIKRPSTGLLMTYLA 288
QY 332 VELCNVLYGFWPFSKTIETDPLSHHYDNNMLPKHGF-----HQMPEKYSQMLQLHMR 385
DB 289 TRFCDEIHLVGFWPFPKDLNGKAVKHYDDL--KYRFSNAPSRMPLEFKTLNVLNHR 346
QY 386 GILKLOFQSKC 395
DB 347 GALKLTGKC 356

RESULT 12

US-09-949-016-10541
; Sequence 10541, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10541
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10541

Query Match 20.0%; Score 419.5; DB 2; Length 429;
Best Local Similarity 28.3%; Pred. No. 3.3e-36;
Matches 116; Conservative 77; Mismatches 180; Indels 37; Gaps 11;
QY 12 GSLMLLLLRMLWCPAD-APARSLLMEGSR-DSGTGSA-----LKTLS----- 56
DB 28 GSRLQALLAFYRPHRDYLPKTEPLYQEKVRELQGLSRAPKRSIRKRWITICTISLL 87
QY 57 ---PTTPVPRNTSYLDEKTTQITEKCKLOYSLSLSNKTTRYSEDDYLTQITNIQRC 113
DB 88 IFYTKTEIARTEE-----HQETQLDGLSLSRSLVNSGDKIIRKAGSSIFO--HNVE-- 139
QY 114 PWRQAEYDNPRAKLASCCDAIQDFVVSQNTPTVTNMSYEVSKEKHIPIRENIFHMP 173
DB 140 GWKINSVLIRKNILPLDRAEDSVVKSFKPGDVIHYVLDRTLNISHDLHSLLP 199
QY 174 VSQPFVDYVYNOCVAVGVGILNKLSCGAEIDKSDPFVFCNLPPITGSKDVGSKTNLV 233
DB 200 EVSPMKNRFFKCAVGVNSGILLDECGKEIDSHNFVIRCNLAPVVEFAA-DVGTGSDFI 258
QY 234 TVNPSIITLYQNLEK--KAQFLDEDISTYDAFLLLPFASVRANTGTSFKYQTLKESK 291
DB 259 TNNPSVVOAFGGFNRSDREKRVHRLSMLNDSVLWIPAFMYKGGKEHVVWVNALILKNK 318
QY 292 NEQVLFPHPRYLRLHALFWRTKGTAYRLSTGLMIASVAVELCNVLYGFWPFSKTIET 351
DB 319 LKVRTAYPSLRSLIHAHVRGYWLTNKNVPIKRPSTGLLMTYLAFCDEIHLVGFWPFPKDLN 378
QY 352 DTPLSHHYDNNMLPKHGF-----HQMPEKYSQMLQLHMRGILKLOFQSKC 395
DB 379 GKAVKHYDDL--KYRFSNAPSRMPLEFKTLNVLNHRGALKTTGKC 426

RESULT 13

US-09-949-016-9465
; Sequence 9465, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9465
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9465

Query Match 19.4%; Score 408.5; DB 2; Length 384;
Best Local Similarity 28.6%; Pred. No. 4.2e-35;
Matches 99; Conservative 64; Mismatches 140; Indels 43; Gaps 7;
QY 84 LOYSLSLSNKTTRYSEDDYLTQITNIORCP-----WNRQAEYD 123
DB 50 IRSVNSLSHKSNR-----AEVINGSSPAVVDNRSNESIKHNIQPASSKWRHNTLSL 103
QY 124 NFRKLASCCDAIQDFVVSQNTPTVTNMSYEVSKEKHIPIRENIFHMPVQPFVDYD 183
DB 104 RIRKQILKFLDAEKDISELVKGTIKPGDIHYIFDRDSTMNVSQNIYELLPTSPKKNKHF 163
QY 184 NQCAVGVNGGILNKLSCGAEIDEDFVFCNLPPITGSKDVGSKTNLVTVNPSIITLK 243
DB 164 GTCALVGVNSGVLLNSGCCQGEIDMSFVIRCNLAPVQEYA-RDVGLKTDLVTVNPSVIO 222
QY 244 YQNL-----KEGQAQFLDEDISTYDAFLLLPFASVRANTGTSFKYQTLKESKMRQKLV 298
DB 223 FEDLVNATWREKLLQRLHSLN--GSILWIPAFMARGGKERVWVNELILKHVNVRTAY 279
QY 299 FHPRYRLHALFWRTKGTAYRLSTGLMIASVAVELCNVLYGFWPFSKTIETDPLSHH 358
DB 280 PSLRLHLAVRGYWLTNKNVPIKRPSTGLLMTYLAFCDEIHLVGFWPFPKDLNQNPNVKYH 339
QY 359 YVDNMLPKHGF-----HQMPEKYSQMLQLHMRGILKLOFQSKCETA 398
DB 340 YDLSL--KIGYTSQASPHMPLFKALKSLHEQGALKUTVGQCDGA 383

RESULT 14

US-08-446-875-8
; Sequence 8, Application US/08446875
; Patent No. 5858751
; GENERAL INFORMATION:
; APPLICANT: Paulson, James C.
; APPLICANT: Wen, Xiaohong
; APPLICANT: Livingston, Brian Duane
; APPLICANT: Gillespie, William
; APPLICANT: Kelm, Serge
; APPLICANT: Burlingame, Alma L.
; APPLICANT: Medzihradsky, Katalin
; TITLE OF INVENTION: Compositions and Methods for the
; IDENTIFICATION AND SYNTHESIS OF SIALYLTRANSFERASES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pons, Smith, Lande & Rose
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: CA

;; COUNTRY: USA
;; ZIP: 90067
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/446,875
;; FILING DATE: July 12, 1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/102,385
;; FILING DATE: August 4, 1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Oldenkamp, David J.
;; REGISTRATION NUMBER: 29,421
;; REFERENCE/DOCKET NUMBER: 111-197
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (310) 788-5000
;; TELEFAX: (310) 277-1297
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 375 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-446-875-8

Query Match 18.5%; Score 389; DB 1; Length 375;
Best Local Similarity 29.3%; Pred. No. 5.2e-33;
Matches 98; Conservative 58; Mismatches 150; Indels 28; Gaps 7;

QY 87 SLNSLNKTRRYSEDDYLOITN-----IQ--RCPMNRQAEYDNFRKILASCCDA 135
DB 47 SLHKSNNRAEVINGSSLPVANSNLSKHSIQPASSKWRHNQTLRLRQKILKFLNA 106

QY 136 IQDFVVSQNNTPVGTNNMSEYVESKKHIPRENIFHMFVPSQPFVDYPYNQCAVVGNGGIL 195
DB 107 EKNISVLKGLKPGNIHIFNRNSTMNVSONLYELLPTSLPKNKHFTQCAIVGNSGVL 166

QY 196 NKSICGAEIDKSDVFRCLNPPITGSAKOVGSKTNLVTNPSIITLKYNL-----KEK 250
DB 167 LNSGCGQEIINTHSFVIRCNLAPVQEYA-RNVGLKTNLVTNPSVIQAFENLVNATWREK 225

QY 251 KAQPLEDISTYGDALLPAPSVANTGISKVKYQTLKESKVRQKVLFFPHRYLRHLALF 310
DB 226 LLQRLHGLN---GSILWIPAFMARGKERVWVNALILKHHVNVRTAYPSLRLLHAVRGY 282

QY 311 WRTKGVYATRLSTGLMIASVAVELCENVKLYGFWPFSTKTIEDTPLSHHYDNNMLPKHGF- 369
DB 283 WLTNKVHIKRPITGLMYTLATRCNQIYLYGFWPFPLNQNDPVKYHYNSL--KYGYT 340

QY 370 -----HOMPKEYSQMLQHLHMRGILKLFQSKCETA 398
DB 341 SQASPTMPLEFKALKSLHEQGALKLTVGQCNGA 374

RESULT 15
US-08-102-385G-8
; Sequence 8, Application US/08102385G
; Patent No. 5962294
; GENERAL INFORMATION:
; APPLICANT: Paulson, James C.
; APPLICANT: Wen, Xiaohong
; APPLICANT: Livingston, Brian Duane
; APPLICANT: Gillespie, William
; APPLICANT: Kelm, Sarge
; APPLICANT: Burlingame, Alma L.
; APPLICANT: Medzihradsky, Katalin
; TITLE OF INVENTION: Compositions and Methods for the
; IDENTIFICATION AND SYNTHESIS OF SIALYLTRANSFERASES
; NUMBER OF SEQUENCES: 36

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
;; STREET: 2029 Century Park East, 38th Floor
;; CITY: Los Angeles
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 90067
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/102,385G
;; FILING DATE: 04-AUG-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/925,669
;; FILING DATE: 04-AUG-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Oldenkamp, David J.
;; REGISTRATION NUMBER: 29,421
;; REFERENCE/DOCKET NUMBER: 97-062
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (310) 788-5000
;; TELEFAX: (310) 277-1297
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 375 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-102-385G-8

Query Match 18.5%; Score 389; DB 1; Length 375;
Best Local Similarity 29.3%; Pred. No. 5.2e-33;
Matches 98; Conservative 58; Mismatches 150; Indels 28; Gaps 7;

QY 87 SLNSLNKTRRYSEDDYLOITN-----IQ--RCPMNRQAEYDNFRKILASCCDA 135
DB 47 SLHKSNNRAEVINGSSLPVANSNLSKHSIQPASSKWRHNQTLRLRQKILKFLNA 106

QY 136 IQDFVVSQNNTPVGTNNMSEYVESKKHIPRENIFHMFVPSQPFVDYPYNQCAVVGNGGIL 195
DB 107 EKNISVLKGLKPGNIHIFNRNSTMNVSONLYELLPTSLPKNKHFTQCAIVGNSGVL 166

QY 196 NKSICGAEIDKSDVFRCLNPPITGSAKOVGSKTNLVTNPSIITLKYNL-----KEK 250
DB 167 LNSGCGQEIINTHSFVIRCNLAPVQEYA-RNVGLKTNLVTNPSVIQAFENLVNATWREK 225

QY 251 KAQPLEDISTYGDALLPAPSVANTGISKVKYQTLKESKVRQKVLFFPHRYLRHLALF 310
DB 226 LLQRLHGLN---GSILWIPAFMARGKERVWVNALILKHHVNVRTAYPSLRLLHAVRGY 282

QY 311 WRTKGVYATRLSTGLMIASVAVELCENVKLYGFWPFSTKTIEDTPLSHHYDNNMLPKHGF- 369
DB 283 WLTNKVHIKRPITGLMYTLATRCNQIYLYGFWPFPLNQNDPVKYHYNSL--KYGYT 340

QY 370 -----HOMPKEYSQMLQHLHMRGILKLFQSKCETA 398
DB 341 SQASPTMPLEFKALKSLHEQGALKLTVGQCNGA 374

Search completed: May 26, 2006, 23:32:27
Job time : 52 secs

Qy 361 DNMLPKHGFHMPKQKYSQMLQHLHMRGILKLOFSKCEA 398
Db 361 DNMLPKHGFHMPKQKYSQMLQHLHMRGILKLOFSKCEA 398

RESULT 2

US-10-501-930-3
; Sequence 3, Application US/10501930
; Publication No. US20060057696A1
; GENERAL INFORMATION:
; APPLICANT: TAKASHIMA, Shou
; APPLICANT: TSUJIMOTO, Masafumi
; APPLICANT: TSUJI, Shuichi
; TITLE OF INVENTION: GLYCOSYLATING ENZYME
; FILE REFERENCE: P25687
; CURRENT APPLICATION NUMBER: US/10/501.930
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: PCT/JP03/00883
; PRIOR FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 3
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Human
US-10-501-930-3

Query Match 84.1%; Score 1768; DB 5; Length 398;
Best Local Similarity 82.4%; Pred. No. 2.5e-159;
Matches 328; Conservative 30; Mismatches 40; Indels 0; Gaps 0;

Qy 1 MRSGGTLFALIGSLMLLLMLWCPADAPARSLLMGSGREDTSGTSAALKTLWSPTTP 60
Db 1 MRPGGALLALLASLLMLLLMLWCPADAPGRARILVEESREATHGTTPAALTLRSPATA 60
Qy 61 VPRFNSYLDKKTQJTEKCDLQYLSNLSNKTREYSEDDYLQTLTIQRCFWRQAE 120
Db 61 VPRATNLYNEKSLQTEKCNLQYLGIESFNKTKYSENDYLIQIITDIQSCPWKQAE 120
Qy 121 EYDNFRKALASCCDAIQDFVVSQNTTVPVTNMSYEVESEKHHIPIRENIHMFVVSQPFVD 180
Db 121 EYANFRKALASCCDAVQNFVVSQNTTVPVTNMSYEVESEKKEIPIKKNIFHMFVVSQPFVD 180
Qy 181 YPNQCAVWNGGILNKLSCGAEIDKSDVFRCLMPLPITGASKDVGSKNLVTNPSII 240
Db 181 YPNQCAVWNGGILNKLSCGTEIDKSDVFRCLMPLPITGSDVSKDVGSKNLVTNPSII 240
Qy 241 TLKYNLKEKKAQFLEIDISTYGDALFLLPAPSYRANTGISFKVYOTLKESKMRQKVLFFH 300
Db 241 TLKYNLKEKKAQFLEIDATYGDALFLPAPSYRANTGTSFKVYOTLKESKMRQKVLFFH 300
Qy 301 PRYLRLHALFWRTKGVTAAYRLSTGLMIASVAVELCENVKLYGFWPFSKTIETPLSHYY 360
Db 301 PKYLKOLALFWRTKGVTAAYRLSTGLMITSVAVELCKNKLKLYGFWPFSKTIETPLSHYY 360
Qy 361 DNMLPKHGFHMPKQKYSQMLQHLHMRGILKLOFSKCEA 398
Db 361 DNMLPKHGFHMPKQKYSQMLQHLHMRGILKLOFSKCEA 398

RESULT 3

US-10-430-325-2
; Sequence 2, Application US/10430325
; Publication No. US20040002138A1
; GENERAL INFORMATION:
; APPLICANT: SASAKI, KATSUTOSHI
; MIURA, KAZUMI
; HANAI, NOBUO
; NISHI, TATSUNARI
; TITLE OF INVENTION: '-2,8-SIALYLTRANSFERASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEES ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/430.325
FILING DATE: 07-May-2005
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361.304A
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: PCT/JP94/00495
FILING DATE: 28-MAR-1994
APPLICATION NUMBER: JP 081-5-69988
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 321955
REFERENCE/DOCKET NUMBER: 249-66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 356
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: WM266-4 cell
CELL TYPE: melanoma
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-430-325-2

Query Match 33.2%; Score 697; DB 4; Length 356;
Best Local Similarity 43.3%; Pred. No. 2.5e-57;
Matches 129; Conservative 60; Mismatches 107; Indels 2; Gaps 2;

Qy 99 SEDYLTQITTIQRCFWRQAEIDNFRKALASCCDAIQDFVVSQNTTVPVTNMSYEVESE 158
Db 53 NEKEIVQGVQLQGTAWRRNQTFRAFRKQMEDCCDPAHLFAMTKMNSPQKSMWYDGEF 111
Qy 159 KGHIPRENIHMFVVSQPFVDYVQCAVWNGGILNKLSCGAEIDKSDVFRCLMPLP 218
Db 112 LYSFTTIDNSTYSLFPQATPF-QPLKKCAVWNGGILKKSQCGRQIDEANFVRCLNPL 170
Qy 219 TGSASQDVSKTNLVTNPSIIITKYONLKEKKAQFLEIDISTYGDALFLLPAPSYRANTG 278
Db 171 SSETKDVGANSQVLTANPSIIIRFQNLWSKTFVNNKITYNHSYIYNPASMKTGTE 230
Qy 279 ISFKVYQTLKESKMRQKVLFFHFIYLRHLALFWRTKGVTAAYRLSTGLMIASVAVELCENV 338
Db 231 PSRLVYVYTLSDVGANQTVLFANEFILRSIGFKWKSRIHAKRLSTGLFLVSAALGLCEEV 290
Qy 339 KLYGFWPFSKTIETDPLSHYYDMLPKHGFHMPKQKYSQMLQHLHMRGILKLOFSKCE 396
Db 291 AIYGFWPFVSVMWHEQPISSHYYDMLPKHGFHMPKQKYSQMLQHLHMRGILKLOFSKCE 348

RESULT 4

US-10-169-989-1
; Sequence 1, Application US/1016989
; Publication No. US20040092438A1
; GENERAL INFORMATION:
; APPLICANT: Martin-Villalba, Ana

```
; APPLICANT: Schenkel, Johannes
; APPLICANT: Kleber, Susanne
; APPLICANT: Testi, Roberto
; TITLE OF INVENTION: USE OF G33-SYNTHASE-INHIBITORS FOR THE TREATMENT OF
; TITLE OF INVENTION: NEUROPATHOLOGICAL DISORDERS AND PROCESS FOR IDENTIFYING
; TITLE OF INVENTION: G33-SYNTHASE-INHIBITORS
; FILE REFERENCE: M/40289
; CURRENT APPLICATION NUMBER: US/10/169,989
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/EP00/12224
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-169-989-1

Query Match      33.2%; Score 697; DB 4; Length 356;
Best Local Similarity 43.3%; Pred. No. 2.5e-57;
Matches 129; Conservative 60; Mismatches 107; Indels 2; Gaps 2;

Qy      99 SEDYLQITITNRCPCMNROAEYDNFRAKLASCDDAIQDFVVSQNTTVPVGTNMSYEYES 158
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      53 NEKEIVQGVLO-QGTATERNQTAARAFKQMEDCCDPAHLFAMTKWNSPMGKSMWYDGEF 111
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      159 KKHPIRENIHFMPVPSQPFVDVYPNQCAVGVNGGILNKSICGABIDKSDFFVRCNLPPI 218
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      112 LYSFTIDNSTYSLFPQATPF-QLPLKCAVGVNGGILKSKGCGROIDBANFVMRCNLPPL 170
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      219 TGSASKDVGSKTNVTVNPSIITLKYONLKEKKAQFLEDISTYCGDAFLLLPFAFSVRANTG 278
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      171 SSETYKDVGAQSQLVANPSIIRQFQNLWSRKTFFVDNMKIYNSIYMPFAFSMKTGTE 230
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      279 ISFKVYQTLKESKMRQKVLFFHPRYLRLHALFWRTKGTAVRLSTGLMIASVAVELCENV 338
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      231 PSLRVYITLSDVGANQTVLPANPNELRISIGKFWKSRGHIHAKELSTGLFLVSAALGLCEV 290
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      339 KLYGFWPFSKTIETDPLSHHYDNNMLPKHGFHQMPKEYSQMLQLHMRGILKQSKCE 396
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      291 AIYGFWPFSVNNHQPISHHYDNNVLPFSGFHAMPEEFQLWLHKGALRMQLDPCE 348
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-10-106-698-5484
; Sequence 5484, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5484
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (25)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (34)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; NAME/KEY: MISC FEATURE
; LOCATION: (50)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5484

Query Match      12.9%; Score 272; DB 4; Length 122;
Best Local Similarity 52.9%; Pred. No. 1.6e-17;
Matches 46; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

Qy      310 FWRTKGTAVRLSTGLMIASVAVELCENVKLYGFWPFSKTIETDPLSHHYDNNMLPKHGF 369
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      28 FWKSRGXHAKELSTGLFLVSALNKLCEVAIYGFWPFSVNNHQPISHHYDNNVLPFSGF 87
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      370 HMPKEYSQMLQLHMRGILKQSKCE 396
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Db      88 HAMPEEFQLWLHKGALRMQLDPCE 114
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RESULT 6
US-09-867-550-1960
; Sequence 1960, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and
; FILE REFERENCE: 21402-013 (Cura-3)
; CURRENT APPLICATION NUMBER: US/09867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USN 60/308,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1960
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-1960

Query Match      10.7%; Score 224; DB 3; Length 50;
Best Local Similarity 86.0%; Pred. No. 1.7e-13;
Matches 43; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      278 GISFKVYQTLKESKMRQKVLFFHPRYLRLHALFWRTKGTAVRLSTGLMI 327
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 GTSFKVYITLESKARQKVLFFHPRYLRLHALFWRTKGTAVRLSTGLMI 50
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RESULT 7
US-09-989-722-347
; Sequence 347, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
```

APPLICANT: Kljavin, Ivar J.	PRIOR FILING DATE: 1998-06-10
APPLICANT: Napier, Mary A.	PRIOR APPLICATION NUMBER: 60/088742
APPLICANT: Pan, James	PRIOR FILING DATE: 1998-06-10
APPLICANT: Paoni, Nicholas P.	PRIOR APPLICATION NUMBER: 60/088870
APPLICANT: Roy, Margaret Ann	PRIOR FILING DATE: 1998-06-10
APPLICANT: Stewart, Timothy A.	PRIOR APPLICATION NUMBER: 60/088874
APPLICANT: Tumas, Daniel	PRIOR FILING DATE: 1998-06-10
APPLICANT: Watanabe, Colin K.	PRIOR APPLICATION NUMBER: 60/088876
APPLICANT: Williams, P. Mickey	PRIOR FILING DATE: 1998-06-10
APPLICANT: Wood, William I.	PRIOR APPLICATION NUMBER: 60/088878
APPLICANT: Zhang, Zemin	PRIOR FILING DATE: 1998-06-11
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	PRIOR APPLICATION NUMBER: 60/088880
TITLE OF INVENTION: Acids Encoding the Same	PRIOR FILING DATE: 1998-06-11
FILE REFERENCE: P2730P1C63	PRIOR APPLICATION NUMBER: 60/088882
CURRENT APPLICATION NUMBER: US/09/989,722	PRIOR FILING DATE: 1998-06-11
CURRENT FILING DATE: 2001-11-19	PRIOR APPLICATION NUMBER: 60/088884
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PRIOR APPLICATION NUMBER: 60/088734	PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/090540
PRIOR APPLICATION NUMBER: 60/088738	PRIOR FILING DATE: 1998-06-24

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; PRIOR APPLICATION NUMBER: 60/088734
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091932
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 10.5%; Score 221; DB 3; Length 600;

Best Local Similarity 30.3%; Pred. No. 1.2e-11;

Matches 69; Conservative 35; Mismatches 96; Indels 28; Gaps 8;

Qy 186 CAVVGGGILNKSILCGAIDKSVFRCNLPPITGSASKDVGSKTNL-----VTVNPSII 240

Db 365 CAVVGGGILNNSHMGQIDSHVTFRLSGALING-YEQDVGTISYFGTAFSLTQSL 423

Qy 241 TLKYQNLK-----KKAQFLADISTYG--DAFLLLPAFSYRANTGISFKVYQTLKESK 291

Db 424 ILNRRGKVPVPLGKDVYHLHFLSTRDYEWLEALLMNTVMSKNLFWFRHRPQAFREAL 483

Qy 292 MRQKVLFFHPRYLHLA-LFWRHGVTA-----YRLSTGLMIASVAVELCENVKLYGFWP 345

Db 484 HMDRYLLLPDPLRYMKNRFLRSLTLDGAHWRIYRPTTGALLLTALQLCDQVSAYGF-- 541

Qy 346 FSKTIEDTPLSHHYDNNLPKHQF---HQPKEYSQMLQLHMRGILKL 390

Db 542 --ITEGHERFSDHYDTSWKRLPYINHDFKLEREVWKRHLHDEGIIRL 587

RESULT 9

US-09-989-279-347

; Sequence 347, Application US/09989279

; Patent No. US20020072496A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Borstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
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53 PRIOR FILING DATE: 1998-07-09

Query Match 10.5%; Score 221; DB 3; Length 600;

Best Local Similarity 30.3%; Prid: No. 1.2e-11;
Matches 69; Conservative 35; Mismatches 96; Indels 28; Gaps 8;

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QY 292 MRQKVLFEHRYLRHLA-LFWRKKGVTG-----YELSTGLMTASVAVELCENKLYGFWP 345
DB 484 HNDRYLLHPDFLRYMKNRFLRSKTLDGAWHMYIRPTTGALLLTLALCQDVSAYGF-- 541
QY 346 FSKTIEDTPLSHYYDNMLPKHCF---HOMPKYEQSMLQLHMRGILKL 390
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Matches	69; Conservative
Mismatches	96; Indels
Gaps	8;

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Db 484 HMDRYLLHDPFLRYMKNRFLRSKTLDDGAHWIRYPTTGALLLTALQLCDQVSAYGF-- 541
QY 346 PSKTIEDTFLSHHYNDMLPKHGF---HOMPKEYSQMLQHLNRGILKL 390
Db 542 --ITEGHERFSDHYDTSWKLIFVINHDFKLREVRWKLHDEGIRL 587

RESULT 13

US-09-991-073-347
; Sequence 347, Application US/09991073
; Patent No. US2002012756A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1997-06-16
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Db	424	ILGNRGPKNPVLGKDVRYLHFLGTRDYEWLEALLMNQTVMSKNLFWFHRRPQEAFFREAL	483	
Qy	292	MROKVLFFHPRYLRLHLA--LFWRTKGVTG-----YRLSTGLMTASVAVELCENVKLYGWP	345	
Db	484	HMDRYLLHPDFLYMKQRFLRSKTLDCGAWHFIYRPTTGALLLLTALQICDOVSAYGP--	541	
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RESULT 15
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; Sequence 347, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: F2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match      10.5%; Score 221; DB 3; Length 600;
Best Local Similarity 30.3%; Pred. No. 1.2e-11;
Matches 69; Conservative 35; Mismatches 96; Indels 28; Gaps 340

QY 186 CAVGVNGGILNKSCLGAEIDKSFPRCNLPPTTGSASKDVGSKTNL-----VTVNPSII 240
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 365 CAVGVNGGILNNSHNGQEIDSHNVFRLSGALIKG-YEQDVGTRTSFYGFAPSLTQSL 423
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 TLKYQNLKE-----KKAQFLDSTYG--DAFLLLPAPSVRANTGISEKVVQTLKESK 291
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 424 ILGNRGFKNVPLGKDVRYLHFLETRDYEWEALLMNQTVMSKNLFWFRRPOEAFREAL 483
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 292 MRQKVLFFHPRYLHLA-LFWRTGVTGVTGTA-----YRLSTGLMTASAVELCENVKLVGF 345
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 484 HMDRYLLHPDLRYMKNRFLSKLGDGHNWRIYRPTTGALLLLTLALQCDQVSAIGF-- 541
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 346 FSKTIEDTPLSHYDNMLPKHGF---HOMPKEYSQMLQHLMRGIILKL 390
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 542 --ITEGHERFSDDHYDTWSKRLLEYINHDFKLEREVWKLHDEGIURL 587
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: May 26, 2006, 23:46:15
Job time : 186 secs

```

Search completed: May 26, 2006, 23:40:15
Job time : 186 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 26, 2006, 23:43:21 ; Search time 15 Seconds
(without alignments)
295.511 Million cell updates/sec

Title: US-10-501-930-1
Perfect score: 2102
Sequence: 1 MRSGTFLALIGSLMLLLL.....MLQLHMRGILKQFSKCFKA 398

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /EMC Celerra_SIDS3/ptodata/1/pubpa/US09_NEW_PUB pep:**
2: /EMC Celerra_SIDS3/ptodata/1/pubpa/US06_NEW_PUB pep:**
3: /EMC Celerra_SIDS3/ptodata/1/pubpa/US07_NEW_PUB pep:**
4: /EMC Celerra_SIDS3/ptodata/1/pubpa/US08_NEW_PUB pep:**
5: /EMC Celerra_SIDS3/ptodata/1/pubpa/PCT_NEW_PUB pep:**
6: /EMC Celerra_SIDS3/ptodata/1/pubpa/US10_NEW_PUB pep:**
7: /EMC Celerra_SIDS3/ptodata/1/pubpa/US11_NEW_PUB pep:**
8: /EMC Celerra_SIDS3/ptodata/1/pubpa/US60_NEW_PUB pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162.5	7.7	252	6	US-10-953-349-22484
2	162.5	7.7	396	6	US-10-953-349-22483
3	162.5	7.7	414	6	US-10-953-349-22482
4	159	7.6	331	6	US-10-505-928-321
5	150.5	7.2	394	6	US-10-953-349-20496
6	150.5	7.2	419	6	US-10-953-349-20495
7	150.5	7.2	435	6	US-10-953-349-20494
8	149	7.1	362	6	US-10-196-749-508
9	138	6.6	287	6	US-10-953-349-12052
10	126	6.0	401	6	US-10-953-349-34787
11	126	6.0	404	6	US-10-953-349-34786
12	123	5.9	299	6	US-10-196-749-206
13	86.5	4.1	210	6	US-10-196-749-536
14	86	4.1	146	7	US-11-293-697-3338
15	86	4.1	544	6	US-10-196-749-274
16	85	4.0	857	6	US-10-505-928-272
17	84	4.0	228	6	US-10-953-349-18479
18	84	4.0	238	6	US-10-953-349-18478
19	84	4.0	250	6	US-10-953-349-18477
20	84	4.0	288	6	US-10-953-349-1224
21	83.5	4.0	340	6	US-10-953-349-18713
22	82	3.9	1842	6	US-10-511-937-2929
23	81	3.9	197	6	US-10-953-349-22878
24	81	3.9	319	6	US-10-953-349-22877
25	81	3.9	341	6	US-10-953-349-22876

ALIGNMENTS

RESULT 1
US-10-953-349-22484
; Sequence 22484, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THEORY
; CURRENT APPLICATION NUMBER: US/10953349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22484
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22484

Query Match 7.7%; Score 162.5; DB 6; Length 252;
Best Local Similarity 26.0%; Pred. No. 4.8e-07;
Matches 56; Conservative 36; Mismatches 84; Indels 39; Gaps 10;

Qy	183	YNOCVVNGGILNKLSCGAEILASDFVRCNLPPITGSAKDYGSKTNLVTNPSIITL	242
Db	29	YSCAVVNGGILNRLDYGSEIDHEFVIRLNARVDHFETK-VGKKTISIFMNSNIIHL	87
Qy	243	KYONLKEKKAQFLIEDISTYGDARALLPAFSVRANTGISFKVYQTLKESKMRQKVLFFHPR	302
Db	88	-----CARRGGCFCH---PYGDR--VFIVMICO-ALHFMDY-TVCNASHKAPLIVTPR	135
Qy	303	Y-----LRLHAL--FWRTKGV-----TAYRLSTGLMIASVAVELCENKLYG	342
Db	136	FDVLCARIVKYSLKRFVRSRGKLEKMGAEHDGSLFHYSSGMQAVMLALGICDRVSIFG	195
Qy	343	FWPFSKTIEDPLSHHYDNMLFHHGHQMPKEYS	377
Db	196	FG-----KTSAKHHYHTNQKALHLHDVEAEYA	224

RESULT 2
US-10-953-349-22483
; Sequence 22483, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THEORY

FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22483
LENGTH: 396
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-22483

Query Match
Best Local Similarity 7.7%; Score 162.5; DB 6; Length 396;
Matches 56; Conservative 36; Mismatches 84; Indels 39; Gaps 10;

183 YNOCAVVGNGGILNKSICGAEIDKSDVFRCLNLPPIITGSASKDVGSKTNLVTNPSIITL 242
173 YSSCAVVGNGGILLNRDYGSEIDSHFVIRLNNARVDHFETK-VGKKTISIFMNSNLIHL 231
243 KYQNLKEKKAQFLEDISTYGDALFLLPAPFSYRANTGISFKYQTLKESKMRQKLVFFHPR 302
232 ---CARRGGCFCH---PYGDR---VPVIMVICO-ALHFMDY-TVCNASHKAPLLVTDPR 279
303 Y-----LRHLAL--FWRTKGV-----TAYRLSTGLMIASVAVELCENVKLYG 342
280 FDLVCARIVKYSLKRFVEESGKLEKGEAHDGSLFHYSSGMQAVMLALGICDRVSIFG 339
343 FWPFSTIEDTPLSHHYDNNMLPKHGFHOMPKES 377
340 FG-----KSTSAKHVHTNOKAELHLHDYEAAYA 368

RESULT 3
US-10-953-349-22482
Sequence 22482, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22482
LENGTH: 414
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-22482

Query Match
Best Local Similarity 7.7%; Score 162.5; DB 6; Length 414;
Matches 56; Conservative 36; Mismatches 84; Indels 39; Gaps 10;

183 YNOCAVVGNGGILNKSICGAEIDKSDVFRCLNLPPIITGSASKDVGSKTNLVTNPSIITL 242
191 YSSCAVVGNGGILLNRDYGSEIDSHFVIRLNNARVDHFETK-VGKKTISIFMNSNLIHL 249
243 KYQNLKEKKAQFLEDISTYGDALFLLPAPFSYRANTGISFKYQTLKESKMRQKLVFFHPR 302
250 ---CARRGGCFCH---PYGDR---VPVIMVICO-ALHFMDY-TVCNASHKAPLLVTDPR 297
303 Y-----LRHLAL--FWRTKGV-----TAYRLSTGLMIASVAVELCENVKLYG 342
298 FDLVCARIVKYSLKRFVEESGKLEKGEAHDGSLFHYSSGMQAVMLALGICDRVSIFG 357
343 FWPFSTIEDTPLSHHYDNNMLPKHGFHOMPKES 377
358 FG-----KSTSAKHVHTNOKAELHLHDYEAAYA 386

RESULT 4

US-10-505-928-321
Sequence 321, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/365,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
SEQ ID NO 321
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-321

Query Match
Best Local Similarity 7.6%; Score 159; DB 6; Length 331;
Matches 63; Conservative 35; Mismatches 80; Indels 68; Gaps 12;

178 FVDYPYNOCAVVGNGGILNKSICGAEIDKSDVFRCLNLPPIITGSASKDVGSKTNLVTNVP 237
110 FDMIPCKCVVVGNGGVLKNKTLIEKIDSVDVIRMNNGPVLGH-EEVGRRRTTFRFLFYP 168
238 SIITLKYQNLKEKKAQFLEDISTYGDALFLLPAPFSYRANTGISFKYQTLKESKMRQKV- 296
169 ESV-----PSDPIHNPNTVILTAFKPHD-----LRWLLELLMGDKIN 207
297 -----LFFHPRYLRLALF-WRTKGVTAAYRL-----STGLMIA 328
208 TNGFWKKPALNLIYKPYQIRILDFIIRT---AAYELLHFPKVPKQKPKHPTTGIITAI 264
329 SVAVELCENVKLYGF-WPFSTIEDTPLSHHYDNNMLPKHGFHOMPKESQMLQLH 383
265 TLAFYICHEVHLAGKYNFSDL--KSPL--HYIGNATMSLMKNQVAYHNVTAE-----QLF 315
384 MRGILK 389
316 LKDIIE 321

RESULT 5
US-10-953-349-20496
Sequence 20496, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 20496
LENGTH: 394
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-20496

Query Match
Best Local Similarity 7.2%; Score 150.5; DB 6; Length 394;
Matches 54; Conservative 36; Mismatches 86; Indels 39; Gaps 10;

183 YNOCAVVGNGGILNKSICGAEIDKSDVFRCLNLPPIITGSASKDVGSKTNLVTNPSIITL 242
171 YSSCAVVGNGGILLNRNRYGSEIDSHFVIRLNNARVDHFETK-VGKKTISIFMNSNLIHL 229
243 KYQNLKEKKAQFLEDISTYGDALFLLPAPFSYRANTGISFKYQTLKESKMRQKLVFFHPR 302

US-10-505-928-321
Sequence 321, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/365,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
SEQ ID NO 321
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-321

Query Match
Best Local Similarity 7.2%; Score 150.5; DB 6; Length 394;
Matches 54; Conservative 36; Mismatches 86; Indels 39; Gaps 10;

183 YNOCAVVGNGGILNKSICGAEIDKSDVFRCLNLPPIITGSASKDVGSKTNLVTNPSIITL 242
171 YSSCAVVGNGGILLNRNRYGSEIDSHFVIRLNNARVDHFETK-VGKKTISIFMNSNLIHL 229
243 KYQNLKEKKAQFLEDISTYGDALFLLPAPFSYRANTGISFKYQTLKESKMRQKLVFFHPR 302

Db 230 ----CARRGGCFCH---PYGDN---VPIVMYICQ-AVHFLDY-TVCNASHKAPLLVTDPR 277
Qy 303 Y-----LRHLAL---FWRTKV-----TAYRLSTGLMTASVAVELCENVKLYG 342
Db 278 FDLVCARIVKYSLKRFVEESGKLEKMGAEHDSLFHYSSGMQAVILALGICDRVSIFG 337
Qy 343 FWPFSTKTIEDTPLSHHYDDNMLPKHGFHQPMPKEYS 377
Db 338 FGKLASA-----KHHYHTNQAEHLHLHDYEAEYA 366

RESULT 6
US-10-953-349-20495
; Sequence 20495, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20495
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20495

Query Match 7.2%; Score 150.5; DB 6; Length 419;
Best Local Similarity 25.1%; Pred. No. 1.1e-05;
Matches 54; Conservative 36; Mismatches 86; Indels 39; Gaps 10;
Qy 183 YNOCVVNGGILNKSLGCAEIKSDFFVRCNLPPITGSASKDVGSKTNLTVNPSIITL 242
Db 196 YSSCAVNGSGILLNRNYGSEIDSHSEVIRLNNARVDHFETK-VGKKTISIFMNSNHL 254
Qy 243 KYONLKEKKAOFLEIDISTYGDALFLLPAPSYRANTGISFKVYQTLKESMRQKVLPFFHPR 302
Db 255 ----CARRGGCFCH---PYGDN---VPIVMYICQ-AVHFLDY-TVCNASHKAPLLVTDPR 302
Qy 303 Y-----LRHLAL---FWRTKV-----TAYRLSTGLMTASVAVELCENVKLYG 342
Db 303 FDLVCARIVKYSLKRFVEESGKLEKMGAEHDSLFHYSSGMQAVILALGICDRVSIFG 362
Qy 343 FWPFSTKTIEDTPLSHHYDDNMLPKHGFHQPMPKEYS 377
Db 363 FGKLASA-----KHHYHTNQAEHLHLHDYEAEYA 391

RESULT 7
US-10-953-349-20494
; Sequence 20494, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20494
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20494

Query Match 7.2%; Score 150.5; DB 6; Length 435;
Best Local Similarity 25.1%; Pred. No. 1.1e-05;
Matches 54; Conservative 36; Mismatches 86; Indels 39; Gaps 10;

Qy 183 YNOCVVNGGILNKSLGCAEIKSDFFVRCNLPPITGSASKDVGSKTNLTVNPSIITL 242
Db 212 YSSCAVNGSGILLNRNYGSEIDSHSEVIRLNNARVDHFETK-VGKKTISIFMNSNHL 270
Qy 243 KYONLKEKKAOFLEIDISTYGDALFLLPAPSYRANTGISFKVYQTLKESMRQKVLPFFHPR 302
Db 271 ----CARRGGCFCH---PYGDN---VPIVMYICQ-AVHFLDY-TVCNASHKAPLLVTDPR 318
Qy 303 Y-----LRHLAL---FWRTKV-----TAYRLSTGLMTASVAVELCENVKLYG 342
Db 319 FDLVCARIVKYSLKRFVEESGKLEKMGAEHDSLFHYSSGMQAVILALGICDRVSIFG 378
Qy 343 FWPFSTKTIEDTPLSHHYDDNMLPKHGFHQPMPKEYS 377
Db 379 FGKLASA-----KHHYHTNQAEHLHLHDYEAEYA 407

RESULT 8
US-10-196-749-508
; Sequence 508, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SCRUTED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 10/052545
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059283
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059285
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063435
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 508
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-508

Query Match 7.1%; Score 149; DB 6; Length 362;
Best Local Similarity 21.7%; Pred. No. 1.2e-05;
Matches 73; Conservative 50; Mismatches 107; Indels 106; Gaps 16;
Qy 97 RYSEDDYLTQITNIGRCFQWNEQES-EYD-----NFRAKLASCCDAIQDFVVVSQNTIPVG 149

Db 80 RYSVD-----LLPFVQKAPDSEASKYDPPGFRKFSKVKQTILLELLP----- 123
Qy 150 TMSYEVSCKHPIRENI FHMFPVSQPFVDYPNQCAVGVNGGILNKS LCGAIDKSD F 209
Db 124 -----EHLDPHLKAK-----TCRRCVVIGSGGILHGLGHTLNQPDV 162
Qy 210 VFRCNLPITGSASQVSKTNLVNPSIITLKQNLKKEKAQFLEDISTYGDFAFLLP 269
Db 163 VIRLNSAPVEG-YSEHVGNKTTIRMTYP-----EGAPLSOLEYYSNDLFVAV 208
Qy 270 AFSYRANTGISFKVYQTL--KESKMRQKVLFF-----HPKYLRLH----- 307
Db 209 LFK-----SVDENLQAMVKETLPFWRLFWKQVASKIPLOKHFILNPVLIKETAP 263
Qy 308 -----ALFW-RTKGVTAIRYSTGLMIASVAVELCENVKLYGFNFPFSKTIETDPLSH 357
Db 264 DILQYSEFQSRFGWRDKNVP---TIGVIAVVLATHLDCVSLAGF-GYDLNQPRTEL-- 316
Qy 358 HYDNNM----LPKHGFFHOMPKKEYSOMLQHLHMRGILK 389
Db 317 HYFDSQCAAMNFOTMHNVTETTKFLKLKLVKEGVVK 352

RESULT 9

US-10-953-349-12052
; Sequence 12052, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12052
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (197)..(192)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (213)..(213)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (224)..(224)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (247)..(247)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (272)..(272)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-12052

Query Match 6.6%; Score 138; DB 6; Length 287;
Best Local Similarity 25.0%; Pred. No. 7.6e-05;
Matches 59; Conservative 36; Mismatches 83; Indels 58; Gaps 10;

Qy 166 ENIFHMPVSPQPFVDYPNQCAVGVNGGILNKS LCGAIDKSD FVFRCNLPITGSASKD 225
Db 2 EKLSLVLPPTPPPPROFGRCAVGVNGGILNKTGFEIDGYEVIRENGAP-TQNYTDY 60
Qy 226 VGSKTNLVNPSIITL--KYQNLKKEKAQFLEDISTYGDFAFLLPAPFSYRANTGISPKV 283
Db 61 VGRKSTTRLLNRSKAKLDKVEEDORKEVLIITKIHTDM----- 102
Qy 284 YQTLKESKMRQKVLFFHPRYLRL--ALFW-RTKGVTAIRYSTGLMIASVAVELCENVKLYG 342
Db 103 -----NKMIREVPKPNPVVLMLEASGSAAKG-----TGLKALEFALSCDSDVMYG 149
Qy 343 F-----HPFSKTIETDPLSHHYDNNMLPKHGFFHOMPKKEYSOMLQHLHMRGILK 390
Db 150 FTVDPGYKEW--TRYFSESQGH-----TPLHG-----RAYQWME--CLGLIKI 190
RESULT 10
US-10-953-349-34787
; Sequence 34787, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34787
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (169)..(169)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-34787

Query Match 6.0%; Score 126; DB 6; Length 401;
Best Local Similarity 24.5%; Pred. No. 0.0013;
Matches 60; Conservative 23; Mismatches 82; Indels 80; Gaps 9;
Qy 186 CAVVNGGILNKS LCGAIDKSD FVFRCNLPITGSASKDVKSKTNLVNPSIITL----- 240
Db 170 CAVVNGSGTLGSGRGAQIDAHILVIRLNNARVAGFAA-DVGATTGVSFVNSNILLHCAV 228
Qy 241 -----TLKYNLKEKAQFLEDI-----STYGDFAFLLP----- 270
Db 229 RSAITAPGCACHPVGRAVPLAMVCPQPAHLDDLALICNATATPESFPFLLVTDARIDALCA 288
Qy 271 -----PSYR---ANTGISFKVYQTLKESKMRQKVLFFHPRYLRLHFWRTKGVTAIRLS 322
Db 289 RIAYYSRRFRVAATG-----CPASNWRTRHDERYFH-----YS 322
Qy 323 TGLMIASVAVELCENVKLYGFN--PFSKTIETDPLSHHYDNNMLPKHGFFHOMPKKEYSOML 380
Db 323 SGLQAVVMALGACDEVSVFGFHAGAK-----HHYHTNKKKELDLHDYEAYQFYR 374
Qy 381 QLEMR 385
Db 375 DLOER 379

RESULT 11

US-10-953-349-34786
; Sequence 34786, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

```
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34786
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (172)..(172)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-34786

Query Match          6.0%; Score 126; DB 6; Length 404;
Best Local Similarity 24.5%; Pred.No. 0.0013;
Matches    60; Conservative   23; Mismatches    82; Indels     80; Gaps      9

Qy       186 CAVVGNGGILNKSLCGAIDKSDFFRCNLPPIITGSASKDVSGSKTNLVTVPNSII----- 240
           |||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
Db        173 CAVVGNSTLLGSGRGAQIDAHDVLRLNNARVAGFAA-DVGATTGVGFVNILLHCVA 231
                                           ::::::::::::
Qy         241 -----TLKYONLKKEKKAOFLEDI-----STVDGAFLLIPA----- 270
           :               :             :
Db        232 RSAITPGCACHPYGRAVPLAMVCQPAAHLLDALICNATATPESPFP LLVTDARIDLALCA 291
                                     ::::::::::
Qy         271 -----FSYR---ANTGISFKYYOTLKESKMQRKVLFPHPRYLHLALFWRTKGVTAYRLS 322
           ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db        292 RIAKYSNRFRVAATG-----OPASNWTRRHDERIFYH-----YS 325
           ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy         323 TGLMIASVAVELCEENVKLGYF--PFISKTIETPLSHHYVNDMLPKGHGMHPKPKEYSQMQL 380
           ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db        326 SGLQAVMVALGCADSEVSFGFGKAPCAK-----HHHTNQKKELDLDHYEAEYQFYR 377
                                   ::::::::::::
Qy         381 QLHW R 385
           |
Db        378 DLOER 382
```

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RESULT 12
US-10-196-749-206
; Sequence 206, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: F3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; CURRENT APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121

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/ PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063485  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 206  
LENGTH: 299  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-196-749-206
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Query Match      5.9%; Score 123; DB 6; Length 299;  
Best Local Similarity    22.1%; Pred.No. 0.0016;  
Matches   51; Conservative   34; Mismatches   76; Indels   70; Gaps     8
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```
Qy      184 NQCAVWGNGILNKSICGAIDKSDFFVRGNLPPIITGSASXDVGSKT----- 230  
Db              :|||:|||:|||:|||:|||:|||:|||:|||:  
          72 HQCVIVSSSHLLGTCKLGPISAECTIRWMDATPG-YRADVGNKTYRVVAHSSVFRV 130  
Qy      231 -----NLVTNPYSIITUKY---QLKKKAQFLIEDISTYGDAFLLLPAFS----- 272  
Db              :|||:|||:|||:|||:|||:|||:|||:|||:  
          131 LRRPOEFVNTRPETVFIFGWPPESMQKPQSGLRVRVIQRAGLVFPNMEAYAVSPGRMRQFD 190  
Qy      273 --YRANTGISFKVVOTLKESMGDKVLFFPHPRYLRLHALFWRKGVTRYRLSTGLMIASV 330  
Db              :|||:|||:|||:|||:|||:|||:|||:|||:  
          191 DLFRGETG-----KDIEPK-----SWSW-----LSHGFTTWVI 217  
Qy      331 AVELCNVKLYGFMP----FSKTEDTPLSHHYDMLPKKHGHOMPKEYSQ 378  
Db              :|||||:|||:|||:|||:|||:|||:|||:|||:  
          218 AVELCDHVHYGVPNYCQRLELRMPHHYYEPKGDECEVTIQNEHSR 268
```

```
RESULT 13  
US-10-196-749-536  
Sequence 536, Application US/10196749  
Publication No. US2006009486A1  
GENERAL INFORMATION:  
APPLICANT: Baker,Kevin P.  
APPLICANT: Chen,Jian  
APPLICANT: Deenooyers,Luc  
APPLICANT: Goddard,Audrey  
APPLICANT: Godowski,Paul J.  
APPLICANT: Gurney,Austin L.  
APPLICANT: Pan,James  
APPLICANT: Smith,Victoria  
APPLICANT: Watanabe,Colin K.  
APPLICANT: Wood,William I.  
APPLICANT: Zhang,Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C340  
CURRENT APPLICATION NUMBER: US/10196,749  
CURRENT FILING DATE: 2002-07-16  
PRIOR APPLICATION NUMBER: 10/052585  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059268  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059268  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063485  
PRIOR FILING DATE: 1997-10-21
```

```
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 536
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-536

Query Match
Best Local Similarity 4.1%; Score 86.5; DB 6; Length 210;
Matches 24; Conservative 18; Mismatches 41; Indels 1; Gaps 1;

QY 163 PIRENIFHMPVSPFVDYDYPYNOCAVGVNGGILNKSLCGAEIDKSDVFRCNLPPIITGSA 222
Db 57 PLRTHYGIINVKTEPQLDCDLCAIVNSGQMGVQKVGNEIDRSSCIWRNNAPTGG-Y 115

QY 223 SKOVGSKTNLVNPSIITLKYN 246
Db 116 EEDVGRMTIRVVSHTSVPLLLKN 139

RESULT 14
US-11-293-697-3338
; Sequence 3338, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3338
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3338

Query Match
Best Local Similarity 4.1%; Score 86; DB 7; Length 146;
Matches 31; Conservative 17; Mismatches 46; Indels 8; Gaps 4;

QY 186 CAVVNGGILNKSLCGAEIDKSDVFRCNLPPIITGSAKDVGSKTNLVNPSIITLKYN 245
Db 6 CALVTSSGHLHRSQSGQIDQTECVRMNDAPTRG-YGRDVGNTSLRVIAHSSI---Q 60

QY 246 NLKPKQAQFLEDISTYGDALFLLPAPSYRANTGISFKVYQTL 287
Db 61 RILNRHDLN--VSQGTVFIFWGPSSYMRBDG-KGQVYNNL 99

RESULT 15
US-10-196-749-274
; Sequence 274, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
```

```
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052588
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059268
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059268
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062258
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063128
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063128
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063488
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063548
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063548
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063548
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 274
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-274

Query Match
Best Local Similarity 4.1%; Score 86; DB 6; Length 544;
Matches 59; Conservative 42; Mismatches 83; Indels 102; Gaps 15;

QY 90 SLSNKTTRYSEDYLOTITNIOCPWNRQAEEDYNFRAKLA-SCCDAIQDFVVSQNTTP- 147
Db 248 SLSREFLLYSPDN-----KRMARNVLKYERLLAESPNHVAEAVIQRPNIPIH 294

QY 148 -----VGTN-----MSYEVSXKHI---PIRENIFHMPVSPFVDY 181
Db 295 LQTRDTYEGLCQTLGSOPTLYQISLYCSYETNSNAYLLQPIRKEVIHLEPYIALYXDF 354

QY 182 -----PYNQCAVVGCGGILNKSL-CGAEIDKSDVFRCNLPPIITGSAKDV 226
Db 355 VDSQAQKIRELAEPMLQRSVVG---EKQLQVEYRISKAWL-----KD- 397

QY 227 GSKTNLVNPSIITLKYN-----NLKPKQAQFLEDISTYGDALFLLPAPS- 272
Db 398 -----TVDPKLVTLNHRIAALTLGLDVRPPYAEYIQ-VVNYGIGGHEPHFDHATSPSS 449

QY 273 --YRANTG---ISFKVYQTLKESMRQKVLV--FHPRYLRLHALFW 311
Db 450 PLYRMKSGNRVATFMVLYLSVEAGATAFIYANLSVPVVRNALFW 495

Search completed: May 26, 2006, 23:46:35
Job time : 17 secs
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